

89/22

From: Slobodyansky, Elizabeth
Sent: Friday, March 14, 2003 3:56 PM
To: STIC-Biotech/ChemLib
Subject: 09/744,125

Please search for case 09/744,125:

EL

SEQ ID NOS: 1 and 2 against commercial and interference databases.

Thank you.

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Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
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Full text: _____
Patent Family: _____
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VENDOR/COST (where applicable)
STN: _____
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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using SW model

Run on: March 27, 2003, 05:22:50 ; Search time 446 Seconds
(without alignments)

US-09-744-125A-1
7841.600 Million cell updates/sec

Title: Perfect score: 1553
Sequence: 1 gaatttcggcacgagggtggg.....aaaaaaaactcgag 1553

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseg_101002:*

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3: /SIDS2/gcadata/geneseq/geneseq-emb1/NA1982.DAT:
4: /SIDS2/gcadata/geneseq/geneseq-emb1/NA1983.DAT:
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23: /SIDS2/gcadata/geneseq/geneseq-emb1/NA2002.DAT:

RESULT 1
ID AA258953
XX AA258953 standard; cDNA; 1553 BP.
AC AA258953;
XX DT 08-MAY-2000 (first entry)
XX DE Human MIF1 protein encoding cDNA (plasmid pCM480).
XX MEK kinase; MEKK interacting forkhead associated protein; MIF1; MEKK; FHA protein; Forkhead associated protein; tumour; angiogenesis; human; psoriasis; cancer; anti-inflammatory; anti-asthmatic; immunosuppressant; vasotropic; neuroprotective; antiarthritic; antiviral; sa.
KW OS Homo sapiens.
XX FH Key
FT mat_peptide 2..1174 /*tag= a
FT Description Human MIF1 protein
PN WO200005362-A1.
XX PD 03-FEB-2000.
XX PF 21-JUL-1999; 99NO-E05142.
PR 21-JUL-1998; 9BUS-0093590.
XX (RHON) RHONE-POULENC RORER SA.
PI Marcireau C, Multon M, Polard-Houset V;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1553	100.0	1553 21 AA258953	Human MIF1 protein
2	1535.8	98.9	1914 21 AA258958	Human MIF1 protein
C	3	414.4	26.7 10579 22 ABA0014	Human nervous syst
C	4	414.4	26.7 10579 22 ABA0045	Human immune/haeema
C	5	414.4	26.7 28995 22 AAK0046	Human nervous syst
C	6	414.4	26.7 28995 22 AAK0046	Human immune/haeema
C	7	414.4	26.7 28995 22 AAK0047	Human immune/haeema
C	8	414.4	26.7 28995 22 AAK05213	Human immune/haeema
9	351.4	22.6	1905 23 ABL02115	Drosophila melanog

XX	WPI; 2000-195102/17.
DR	P-PDB; AAY77554.
XX	New MEK kinase interacting forkhead associated protein (MIF1) useful to treat or diagnose, e.g. inflammation and tumors, and to identify its specific modulators, to regulate MEK kinase activity -
PT	Claim 3; Page 64-67; 78pp; English.
XX	The invention provides MEK kinase (MEKK) interacting forkhead associated (FHA) protein (MIF1). MIF1 is useful for screening for specific modulators (potential therapeutic agents) and to reduce MEKK activity in cells. Antibodies specific to MIF1 are useful as diagnostic immunoassay reagents to detect expression of MIF1, for purification of MIF1 and as therapeutic (ant)agonists. The MIF1 nucleic acids are useful for: recombinant production of MIF1, either in cultured cells or in vivo (gene therapy); as source of probes and primers for detecting or quantifying genomic DNA encoding MIF1 or expression of mRNA encoding MIF1; as source of therapeutic antisense sequences (used to increase MEKK activity in cells); and to identify inhibitors of MIF1. Regulation of MEKK activity via MIF1 regulation is useful for treatment of inflammation, asthma, immunosuppression, cardiac ischemia or hypertension, myelodysplastic syndrome, neurodegeneration, tumors, angiogenesis, rheumatoid arthritis, psoriasis or persistent viral infections. The present sequence represents a cDNA (plasmid pCM480) encoding a MIF1 protein.
PS	Sequence 1553 BP; 367 A; 457 C; 423 G; 306 T; 0 other;
XX	Query Match Best Local Similarity 100.0%; Score 1553; DB 21; Length 1553; Matches 1553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GATTCGGACGAGGTGGTGGACAGGGCTGTTGGGGTGAACCCCTCTCCG 60
DB	1 GATTCGGACGAGGTGGTGGACAGGGCTGTTGGGGTGAACCCCTCTCCG 60
QY	61 TGAGAAAGAAGGTATCAAAGCCCCCGACACTCTGCCCCACAGCCAGC 120
DB	61 TGAGAAAGAAGGTATCAAAGCCCCCGACACTCTGCCCCACAGCCAGC 120
QY	121 CCTGGACTCACCAAGCGGTGTGAGAAGAGCTAACAGCCACTTCAGG 180
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QY	181 GGGCGTGTGAACTGACCTCTGCTATAATGCTGTCAGACCAACCA 240
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QY	241 CCTGACCTCGTCACCTGGCGTAATCAGTCGGCTTACCCCTGGAGGTCA 300
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QY	301 GGAGCGTGTGAACTGACCTGGCTTACGATCTGCTCAAGTTGGCTGTAGGCC 360
DB	301 GGAGCGTGTGAACTGACCTGGCTTACGATCTGCTCAAGTTGGCTGTAGGCC 360
QY	361 GAGGCAGTGACCGAGGCTATGACGACATCGACGAAAGCCCTTTAACAGC 420
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QY	421 TGAGGAGGCTGTGACGACGACCTGATGCCTCTACTGGCGCTTACGGAGCTCA 480
DB	421 TGAGGAGGCTGTGACGACGACCTGATGCCTCTACTGGCGCTTACGGAGCTCA 480
QY	481 GGACCTGCTGACGACGACCTGATGCCTCTACTGGCGCTTACGGAGCTCA 540
DB	481 GGACCTGCTGACGACGACCTGATGCCTCTACTGGCGCTTACGGAGCTCA 540
QY	541 GGCCACTGCGACTCATGAGGATATTACCTGCTGGGGACAGACGCTGAGCCCT 600
DB	541 GGCCACTGCGACTCATGAGGATATTACCTGCTGGGGACAGACGCTGAGCCCT 600
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AZ5858	601 GCCCAAGGAGCACCAAGTGTGAACTCTCTGATGAGGACCTATGTGAGCACTA 661 GCTCAGGACTGCGAGATGGCTTGTGACATGAGTGTGAGCTGCTGAGCGGCC
ID	601 GCCCAAGGAGCACCAAGTGTGAACTCTCTGATGAGGACCTATGTGAGCACTA 661 GCTCAGGACTGCGAGATGGCTTGTGACATGAGTGTGAGCTGCTGAGCGGCC
XK	661 GCTCAGGACTGCGAGATGGCTTGTGACATGAGTGTGAGCTGCTGAGCGGCC
AC	661 GCTCAGGACTGCGAGATGGCTTGTGACATGAGTGTGAGCTGCTGAGCGGCC
XX	721 GAAGGGAGAGATTGCCAGCTGGAGACAGGAACATGCTGATGGCTGAGGGAC 721 GAAGGGAGAGATTGCCAGCTGGAGACAGGAACATGCTGATGGCTGAGGGAC
QY	721 GAAGGGAGAGATTGCCAGCTGGAGACAGGAACATGCTGATGGCTGAGGGAC 721 GAAGGGAGAGATTGCCAGCTGGAGACAGGAACATGCTGATGGCTGAGGGAC
Db	781 CATCAAGGGATGAGCTCTGGGACATGAGACACAGACAGCTGGAGCTGCTGGGGAC 781 CATCAAGGGATGAGCTCTGGGACATGAGACACAGACAGCTGGAGCTGCTGGGGAC
Db	841 CATGGTGGGACTCTGATGCTGCTGGAGATACACCTGGCAGAGCAACAGATA 841 CATGGTGGGACTCTGATGCTGCTGGAGATACACCTGGCAGAGCAACAGATA
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QY	1321 AGGGCTGGCCATTGAGGCAAGGAGGCTGAGAACCTCAGGCTTCCCTACATCCGA 1321 AGGGCTGGCCATTGAGGCAAGGAGGCTGAGAACCTCAGGCTTCCCTACATCCGA
Db	1321 AGGGCTGGCCATTGAGGCAAGGAGGCTGAGAACCTCAGGCTTCCCTACATCCGA 1321 AGGGCTGGCCATTGAGGCAAGGAGGCTGAGAACCTCAGGCTTCCCTACATCCGA
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QY	1441 ACCTGACTCTGCTGCTGAGCTCTGAGCTTGTGTTATGTTCTT 1441 ACCTGACTCTGCTGCTGAGCTTGTGTTATGTTCTT
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DT	08-MAY-2000 (first entry)

DE Human MIF1 protein encoding cDNA (plasmid pCM577).
 XX
 KW MEK kinase; MEKK interacting forkhead associated protein; MIF1; MEKK;
 KW FHA protein; forkhead associated protein; tumour; angiogenesis; human;
 KW psoriasis; cancer; anti-inflammatory; anti-asthmatic; immunosuppressant;
 KW vasoconstrictive; neuroprotective; antiarthritic; antiviral; ss.
 XX OS Homo sapiens.

XX
 PH Location/Qualifiers
 FT CDS 147..1535 /*tag= a
 PN WO200005362-A1.
 XX PR 03-FEB-2000.
 XX PA (RION) RHONE-POULENC RORER SA.
 XX PT Marcireau, C., Mulon, M., Pollard-Housset, V;
 XX WPI: 2000-195102/17.
 DR P-PSDB; AAY77555.
 XX PT New MEK kinase interacting forkhead associated protein (MIF1) useful to
 PT treat or diagnose, e.g. inflammation and tumors, and to identify its
 PT specific modulators, to regulate MEK kinase activity -
 XX PS Claim 5; Page 70-73; 7BPP; English.
 XX
 CC The invention provides MEK kinase (MEKK) interacting forkhead associated
 CC modulators (potential therapeutic agents) and to reduce MEKK activity in
 CC cells. Antibodies specific to MIF1 are useful as diagnostic immunoassay
 CC reagents to detect expression of MIF1, for purification of MIF1 and as
 CC therapeutic (ant)agonists. The MIF1 nucleic acids are useful for:
 CC recombinant production of MIF1, either in cultured cells or in vivo (gene
 CC therapy); as source of probes and primers for detecting or quantifying
 CC genomic DNA encoding MIF1 or expression of mRNA encoding MIF1; as source
 CC of therapeutic antisense sequences (used to increase MEK activity in
 CC cells); and to identify inhibitors of MIF1. Regulation of MEK activity
 CC via MIF1 regulation is useful for treatment of inflammation, asthma,
 CC immunosuppression, cardiac ischemia or hypertension, myelodysplastic
 CC syndrome, neurodegeneration, tumours, angiogenesis, rheumatoid arthritis,
 CC psoriasis or persistent viral infections. The present sequence represents
 CC a cDNA (plasmid pCM577) encoding a MIF1 protein.
 XX SQ Sequence 1914 BP; 449 A; 549 C; 534 G; 382 T; 0 other;

Query Match 98.9%; Score 1535.8; DB 21; Length 1914;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 75 TATCCAAAGCCCCAGCACTCTGTGCCAOCACCCAGCCCCAGCCCTGGACTACCA 134
 Db 436 TATCCAAAGCCCCAGCACTCTGTGCCAOCACCCAGCCCCAGCCCTGGACTACCA 495
 QY 135 AGCGTGTGAGAGAGTAACAGCCACTCAGGGACCRAGGAATCTGGCCGCTGGAGC 194
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 QY 195 CTSCAAAGACCTCTGTCAATAATGCTGCTGAGAACGACCTGACTTCGTRC 254
 Db 556 CTGAGATGACCTCTGTCAATAATGCTGCTGAGAACGACCTGACTTCGTRC 615

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 Db 1516 CGAATGACACACAGTGGAGATGGGGAGACTCTGGCCCTCTGGCGCTTT 1575
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 Db 1576 CCCTGGCACTCCAGCCGCTTCACTGGAGACTCATGGCTCTGGAAAACCTGGGAGT 1635
 QY 1275 GGAGGGCTCACTGGGGCCATGATGGGGAGATGGGGCTGGCCCTTG 1334
 Db 1636 GGAGGGCTCACTGGGGCCATGATGGGGAGATGGGGCTGGCCCTTG 1695
 QY 1335 TGAGCCAGCAAGGCTGAGAACCTCAGGCTTCCCTAGATCCAGAGGCCCTCCCCATCTT 1394

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Db	1756	CCTCTCTCTAAACACCCCTACCCCATCTACCCCCATGGCACCTCACCTGT 1815	PR	23-AUG-2000; 2000US-0227009.
QY	1455	GTCCTCAGCTGATGATGCCCTAGACTCTCTCTTTATGTGTTCTCTTGAAATAAAGC 1514	PR	30-AUG-2000; 2000US-0228924.
Db	1816	GTCCTCAGCTGATGATGCCCTAGACTCTCTCTTTATGTGTTCTCTTGAAATAAAGC 1875	PR	01-SEP-2000; 2000US-0229287.
QY	1515	ACCAGGTCCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGC 1553	PR	01-SEP-2000; 2000US-0229343.
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XX			PR	08-SEP-2000; 2000US-0231242.
AC			PR	08-SEP-2000; 2000US-0231243.
XX			PR	08-SEP-2000; 2000US-0231244.
DT	23-JAN-2002	(first entry)	PR	08-SEP-2000; 2000US-0231413.
XX			PR	08-SEP-2000; 2000US-0231414.
DE		Human nervous system related polynucleotide SEQ ID NO 12345.	PR	08-SEP-2000; 2000US-0232080.
XX			PR	08-SEP-2000; 2000US-0232081.
KW		Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerability; anti-parkinsonian; antisickling; antianemic; antiarthritic; cancer; anti-rheumatic; hepatotropic; cerebroprotective; anti-inflammatory; anti-allergic; antidiabetic; anticonvulsant; antifungal; antiparasitic; cardiotonic; immune disorder; anticonvulsant; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.	PR	12-SEP-2000; 2000US-0231968.
KW			PR	14-SEP-2000; 2000US-0232337.
KW			PR	14-SEP-2000; 2000US-02323398.
KW			PR	14-SEP-2000; 2000US-02323399.
KW			PR	14-SEP-2000; 2000US-0232400.
KW			PR	14-SEP-2000; 2000US-0232401.
KW			PR	14-SEP-2000; 2000US-0233063.
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PF			PR	29-SEP-2000; 2000US-0236370.
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PR	04-FEB-2000;	2000US-0180028.	PR	02-OCT-2000; 2000US-0237038.
PR	24-FEB-2000;	2000US-0184664.	PR	02-OCT-2000; 2000US-0237039.
PR	02-MAR-2000;	2000US-0186350.	PR	02-OCT-2000; 2000US-0237040.
PR	16-MAR-2000;	2000US-0189874.	PR	13-OCT-2000; 2000US-023935.
PR	17-MAR-2000;	2000US-0190076.	PR	13-OCT-2000; 2000US-0239937.
PR	18-APR-2000;	2000US-0198123.	PR	20-OCT-2000; 2000US-0240960.
PR	19-MAY-2000;	2000US-0205515.	PR	20-OCT-2000; 2000US-0241785.
PR	07-JUN-2000;	2000US-0209467.	PR	20-OCT-2000; 2000US-0241786.
PR	28-JUN-2000;	2000US-0214886.	PR	20-OCT-2000; 2000US-0241787.
PR	30-JUN-2000;	2000US-0215335.	PR	20-OCT-2000; 2000US-0241808.
PR	07-JUL-2000;	2000US-0216147.	PR	20-OCT-2000; 2000US-0241809.
PR	11-JUL-2000;	2000US-0217487.	PR	20-OCT-2000; 2000US-0241826.
PR	14-JUL-2000;	2000US-0218290.	PR	01-NOV-2000; 2000US-0242121.
PR	26-JUL-2000;	2000US-0220363.	PR	08-NOV-2000; 2000US-0244617.
PR	26-JUL-2000;	2000US-0220964.	PR	08-NOV-2000; 2000US-0244619.
PR	14-AUG-2000;	2000US-0224518.	PR	08-NOV-2000; 2000US-0244647.
PR	14-AUG-2000;	2000US-0224519.	PR	08-NOV-2000; 2000US-0244677.
PR	14-AUG-2000;	2000US-0225213.	PR	08-NOV-2000; 2000US-0246522.
PR	14-AUG-2000;	2000US-0225214.	PR	08-NOV-2000; 2000US-0246524.
PR	14-AUG-2000;	2000US-0225216.	PR	08-NOV-2000; 2000US-0246525.
PR	14-AUG-2000;	2000US-0225267.	PR	08-NOV-2000; 2000US-0246526.
PR	14-AUG-2000;	2000US-0225368.	PR	08-NOV-2000; 2000US-0246527.
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PR 18-APR-2000; 2000US-0198123.
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 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
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 PR 22-AUG-2000; 2000US-0226588.
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 PR 14-AUG-2000; 2000US-0225758.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
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 PR 05-SEP-2000; 2000US-0229509.
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 PR 06-DEC-2000; 2000US-0251479.
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 PR 08-DEC-2000; 2000US-051186.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI: 2001-483426/52.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis - Disclosure: SEQ ID NO 24857; 3071pp + Sequence Listing; English.

XX AAK64951 to AAK6702 encode the human immune/hematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)

CC

CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 sequences from the present invention, AAK5492 to AAK5490 and AAM2169 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 10579 BP; 2298 A; 2894 C; 3129 G; 2258 T; 0 other;

Query Match: Best Local Similarity 81.6%; Pred. No. 1.1e-92; Matches 560; Conservative 0; Mismatches 1; Indels 125; Gaps 2;

QY 958 AGGTGTCATCAAGCTGAGNACACGGGATTCCTCATGGCAATGGGGCGAGGCC 1017
Db 10005 AGGTGTCATCAAGCTGAGNACACGGGATTCCTCATGGCAATGGGGCGAGGCC 9946
QY 1018 CATCTACATCAGATGCGACGGCGGCTGCTCTGAGCTTAAATGGCCCTCAGCACACTC 1077
Db 9945 CATCTACATCAGATGCGACGGCGGCTGCTCTGAGCTTAAATGGCCCTCAGCACACTC 9886
QY 1078 TGTGTGTGG-----
Db 9985 TGTGTGTGGAGGTGAGCTGGGGAGGGAGGGAGGAAGGCCAGGATGAGACCTAGGGTGTGA 9826
QY 1086 -----
Db 9825 GCCAGTACACCAACTGGCTCTGGCTCACTCTGTCTTAAGGCACCTTGTCTCCACC 9766
QY 1086 -AGATCGCCAGCCCTGGGATTCGTCCTCCCTATCACACAGACCTTATGCCCTCATCAGG 1144
Db 9765 CAGATGCCAGCTGGGATTCGTCCTCCCTATCACACAGACCTTATGCCCTCATCAGG 9706
QY 1145 GCTGAGGCTGCCAAGATCACACCAAGCTGGAGATGGTGGCAGAACCTGGGCTCTC 1204
Db 9705 GCTGAGGCTGCCAAGATCACACCAAGCTGGAGATGGTGGCAGAACCTGGGCTCTC 9646
QY 1205 CGGCCTGTTCCCTGCCACTCCAGGCCCTTGAGCTGGAAATCAGGCTCCCTGGAAAA 1264
Db 9645 CGGCCTGTTCCCTGCCACTCCAGGCCCTTGAGCTGGAAATCAGGCTCCCTGGAAAA 9586
QY 1325 CTGGCTTGTGAAAGCCAGCAGGGCTGAGAACCTGGGCTCCCTAGTGGAGGAGTAGGG 1324
Db 9525 CTGGCTTGTGAAAGCCAGCAGGGCTGAGAACCTGGGCTCCCTAGTGGAGGAGTAGGG 9466
QY 1385 TCCCCATCTCTCTCTCTAAACACACCTACCCCATCTACCCCATCTACCCCATCTACCT 1444
Db 9465 TCCCCATCTCTCTCTCTAAACACACCTACCCCATCTACCCCATCTACCTACCT 9418
QY 1505 ATAAAGAACCGGGTCCAAGTA 1530
Db 9357 ATAAAGAACCGGGTCCAAGTA 9332

RESULT 5
ID ABA20015
PR 08-SEP-2000; 2000US-0231414.
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PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-02302080.

XK ABA20015;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 12346.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; viricide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; anti-sickling; antihaemolytic; anticarthartic; cancer;
KW antiarthritic; hepatotropic; cerebroprotective; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW antidiabetic; analgesic; antihistaminic; anticonvulsant; antifungal;
KW antiallergic; antidiabetic; antihistaminic; anticonvulsant; antifungal;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX OS Homo sapiens.
XX PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PP 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190075.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
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PR 14-AUG-2000; 2000US-0225265.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
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PR 05-SEP-2000; 2000US-0230437.
PR 01-SEP-2000; 2000US-0230438.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.

Db 19525 GCTGAGGGTCCCAGATCACACCAAGCTAGGAGCTGGGGCAGCTGTGGCCCTCTC 19466
 QY 1205 CGGCGCTGTTCCCTGCCTGACTCCAGGCCCTTGAGCTGGAACTCGTGGCTCCGGAAA 1264
 Db 19465 CGGCGCTGTTCCCTGCCTGACTCCAGGCCCTTGAGCTGGAACTCGTGGCTCCGGAAA 19406
 QY 1265 CCTGGGCACTGGGAAGCTAGCTGGGGCATGGTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1324
 Db 19405 CCTGGGCACTGGGAAGCTAGCTGGGGCATGGTGGGGCTGGGGCTGGGGCTGGGG 19346
 QY 1325 CTGGCCTTGTGAAGCAGCAGGAGGCTGAGAACCTCAGCTTCAGGTTCCCTAGATCCAGAGCCCC 1384
 Db 19345 CTGGCCTTGTGAAGCAGCAGGAGGCTGAGAACCTCAGCTTCAGGTTCCCTAGATCCAGAGCCCC 19286
 QY 1385 TCCCGCATCTCCCTCTCTAAACACACCTACCCCATGCCCTACCCCATGCCCT 1444
 Db 19285 TCCCGCATCTCCCTCTCTAAACACACCTACCCCATGCCCTACCCCATGCCCT 19238
 QY 1445 TCACCTCTGTCTCCAGCTGATNGCTCAGACTCTCTTTATGTGTTCTTGT 1504
 Db 19237 TCACCTCTGTCTCCAGCTGATNGCTCAGACTCTCTTTATGTGTTCTTGT 19178
 QY 1505 AATAAAAGCACCAGGTCCAAGTA 1530
 Db 19177 AATAAAAGCACCAGGTCCAAGTA 19152

RESULT 6

ID AAK70046/c
 XX AAK70046 standard; DNA; 28995 BP.
 AC XX
 DT XX 06-NOV-2001 (first entry)
 DE Human immune/haemopoietic antigen genomic sequence SEQ ID NO:24858.
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytosolic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 PN WO200157182-A2.
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01354.
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0188350.
 PR 16-MAR-2000; 2000US-0188874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0217496.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0235447.
 PR 14-AUG-2000; 2000US-0225758.
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 PR 05-SEP-2000; 2000US-0229513.
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 PR 08-SEP-2000; 2000US-0232201.
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 PR 14-SEP-2000; 2000US-0233065.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
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 PR 14-SEP-2000; 2000US-0233065.
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 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-023544.
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PS Disclosure; SEQ ID NO 34779; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I), by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases or haematopoietic-derived cells. AAK64703 to AAK87634 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.

XX

SQ

Query	Match	Length	Score	DB	Best Local Similarity	Matches	Similarity	Pred.	Mismatches	Indels	Gaps	Other
Qy	958 AGGTCATCAAGCTGAAGACAAAGGTATTCTCATGCCAATGAGGGTCAAGGCC	1017	26.7%	DB	9171 AGGTCATCAAGCTGAAGACAAAGGTATTCTCATGCCAATGAGGGTCAAGGCC	9230	91.6%	92	0	1	2	
Qy	1018 CATCACATCGATGACGGCGGCTCTGGCCCTCAAATGGCCCTAGCAAACTC	1077	26.7%	DB	9231 CATCACATCGATGACGGCGGCTCTGGCCCTAGCAAACTCAGCAAACTC	9290	91.6%	92	0	1	2	
Qy	1078 TGTGGTGG-----	1085	26.7%	DB	9291 TGTGGTGGAGGTGAGGGAGGGAGGAGGATGAGACTTAGGGTGGTGA	9350	91.6%	92	0	1	2	
Qy	1086 -----	1085	26.7%	DB	9351 GCCAGTACACCAACTTGGTCCTGGCACCTCTCTTAAGCCACCTTGTCCTCCACC	9410	91.6%	92	0	1	2	
Qy	1086 -AGATGGCCAACTCGGATGCTCTCTATCACCAACGACTCTATGCCCTCTCAGG	1144	26.7%	DB	9411 CAGATGCCAGCTCTGGATCTGTCCTCTATCACCAACGACTCTATGCCCTCTCAGG	9470	91.6%	92	0	1	2	
Qy	1145 GCTGAGGCTCAAATCACCAACGAGCTGAGGAATGTTGGCAGGAGCTCGTGGCCCTCTC	1204	26.7%	DB	9471 GCTGAGGCTGCAAATCACCAACGAGCTGAGGAATGTTGGCAGGAGCTCGTGGCCCTCTC	9530	91.6%	92	0	1	2	
Qy	1205 CGGCCTGTTCCCTGCCACTCCAGCCGCCCTGACTGGGAACTCTGGCTCTGAA	1264	26.7%	DB	9531 CGGCCTGTTCCCTGCCACTCCAGCCGCCCTGACTGGGAACTCTGGCTCTGAA	9590	91.6%	92	0	1	2	
Qy	1325 CTGGCCTTGTGAACCCAGCAGGAGGCTGAGAACCTCAGGCTCCCTAGATCCAGGCC	1384	26.7%	DB	9651 CTGGCCTTGTGAACCCAGCAGGAGGCTGAGAACCTCAGGCTCCCTAGATCCAGGCC	9710	91.6%	92	0	1	2	
Qy	1385 TCCCCATCT	1444	26.7%	DB	9711 TCCCCATCT	9738	91.6%	92	0	1	2	
Qy	1445 TCACCT	1504	26.7%	DB	9759 TCACCT	9818	91.6%	92	0	1	2	
Qy	1505 AATAAAAGCAGCAGGCTTCAAAGTA	1530	26.7%	DB	9819 AATAAAAGCAGCAGGCTTCAAAGTA	9844	91.6%	92	0	1	2	

CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 Sequence 1905 BP; 490 A; 568 C; 466 G; 381 T; 0 other;
 SQ

Query Match 22.6%; Score 351.4; DB 23; Length 1905;
 Best Local Similarity 60.8%; Pred. No. 2.5e-77; Indels 6; Gaps 2;
 Matches 609; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

QY 1205 CGGCTGTTCCTGCCACTCCACCCCCCTGACTGGGAACTAGGCTCTGAAA 1264
 Db 9531 CGGCCTGTTCCCTGCCACTCCACCCCCCTGACTGGGAACTAGGCTCTGAAA 9590

QY 1265 CCTGGCAGGGGAGCTCACTGGGGCATTTGAGCTTGGGAGGATAGGG 1324
 Db 9591 CCTGGCAGGGGAGCTCACTGGGGCATTTGAGCTTGGGAGGATAGGG 9650

QY 1325 CTGGCTTGGAGCCAGAGGCTGAGGCTTGGGGCATTTGAGCTTGGGAGGATAGGG 1384
 Db 9651 CTGGCTTGGAGCCAGAGGCTGAGGCTTGGGGCATTTGAGCTTGGGAGGATAGGG 9710

QY 1385 TCCCACCTCTCTCTCTAAACACCCATACCCCCATTSCACCT 1444
 Db 9711 TCCCACCTCTCTCTCTAAACACCCATACCCCCATTSCACCT 9758

QY 1445 TCACTCTGCTCAGCTGAGCTTGGGAGGCTGAGCTTGGGAGGATAGGG 1544
 Db 9759 TCACTCTGCTCAGCTGAGCTTGGGAGGCTGAGCTTGGGAGGATAGGG 9818

QY 1505 ATAAAGGACCAAGTTCAGAAGTA 1530
 Db 9819 ATAAAGGACCAAGTTCAGAAGTA 9844

RESULT 9

ABL02115
 ID ABL02115 standard; cDNA; 1905 BP.
 AC XX
 DT ABL02115;
 XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 827.
 KW pharmaceutical; gene; ss.
 OS Drosophila melanogaster.
 PN WO20171042-A2.
 XX PD 27-SEP-2001.
 XX PR 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 DR WPI; 2001-656860/75.
 DR P-PSDB; ABB58012.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 XX Claim 1; SEQ ID NO 827; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB01840-ABL16175) and the encoded proteins (ABB7737-ABB72072).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Db 1026 TTGTTACAGCTGGAGGAGGATCTGCGTGGCACCAATAAGCTCGAACAA 1085
 QY 466 CTTGGAGACCTTCCAGGACCTGTCAGAGCACCCGTGATGCCCTACGTGCGCGTAC 525
 Db 1086 ACTTGAGCACTTCCAGGAGCTACTGATAGAATAGAACTCTCGTTCTACTGCGCGTAC 1145
 QY 526 CGCGAGGCCGCTGAGGCCACTSGCAGCTCATGAGCTATTAACCTGCTGGAGGACA 585
 Db 1206 GTCACTGAAGCTATATGGAGGATCRGAGCCACTCGACCTCTCGATGAGCTCGGGATCA 1205
 QY 643 CTCGATGATGACTAAGCTCAAGGACATGCGAGATGAGGCTCTGAGAATGAGCTGAT 702
 Db 1266 TCAAATCTGGAGCACGACCTGAGGACCAAGCTGAGGAGCTGAGGAGCTGAGATGGGAGC 1325
 QY 703 GTGAGCTGACGGCCGAGAGGAGGATTCGAGCTGAGGAGCTGAGGAGCTGAGATGG 762
 Db 1326 TCTGGCAGATGTCACAAACAAACGTAATATTGCGCTGAGGAGACGAGCTCGGGCTG 1385
 QY 763 GCAGGCTCTAGGGACAGGATCACAGGCTGAGCTCTCG--GACTTGACACAGAC 819
 Db 1386 GGCGCGTCCTGTCGATTCGGCTAGTCGAGGCTGCTCCGAGTTGACACAGAC 1445
 QY 820 ACTGGCAGTCCTGGAGGGCGCATGGGGTACCTGATGCGCTGGCTGAGATCACCT 879
 Db 1446 ACTGGCCTGCTGTTGGCGCTGTTGTTGAGGAAATAACATT 1505
 QY 880 GGGCAGAGCAACGAGGATPACCGATGTTGAGGATGTTGAGGAGGCTG 939
 Db 1506 TGGTCGGATGCCAGGACTGTTGGAGGACGCTGCTGGGGCTGAGGGACGGCTGC 1565
 QY 940 GAAGATATCCGGAAACAGGTCATCACTGGAGGAGGAACTGGTGTCTGGAGGGCTG 999
 Db 1566 GAAGATCTCTGGCCCAAGGACCATTTAGCTGCGAGCATGGGATTTCTCATGC 1625
 QY 1000 CAATGGGGTGGACGCCAACTACATCGATGGAGCCGGCTGCTGGCTCAATG 1059
 Db 1626 TAACGGGAAAGGGCTTATCGAGGCTGACTCTTGTGAGGATTCGGCTG 1685
 QY 1060 GGGCTCAGCAACTCTGGTGGAGATGCCAGCCCTGGCTTCTTATCAA 1119
 Db 1686 TGGACTCGGTCACATGCGAGTGAATAATCCGGCTGGCTCACCTCTGGTCA 1745
 QY 1120 CCAGGACTCATGCCCTCATCAGGGCTGAGGCTGCCAAGA 1160

DB	1746	CTTGAGCTGATCAGCCATTCCGCCAGAGCCAAAG	1786
QY	406	CCTGTTAGCAGGCTGAGGAGCAGCTGCTGAGCAAATG-----	444
DB	1939	TTTGACAGCGTGCAGGAGGATCTGCTGACCATAAGAGCGTAAGTACATT	1880
QY	445	-----GGGTGACGCCAGGCCCCC 466	
DB	1879	TTCATCATGATTTAAGCTTCTAATCAGTAATTCATTCACTCAGTCGAACTAACAAA	1820
QY	467	TGGAGACTCCAGGACCTGTCAGACAGACCCCTGATGCCTTACCTGGCCGTRAC	526
DB	1819	GTCAGCAGTCAGGACTCTGATTAAGATGCCCTTGCTCTCAAGAGTACCCCTGCGATG	1760
QY	527	GCGAAGCCCTGAGCCACTGTCAGCTCATGAGGAGTATTACCTGAGGACAG 586	
DB	1759	GCCAACTCTGCAAAACATGGCTCTCTCAAGAGTACCCCTGCGATG	1700
QY	587	ACAGTCAGGCT --GCCAAAGGGGAGCAGTGTGAAATTCTGATCAGGAGCAC 63	
DB	1699	TCACTGAGCCPATATGGCACGAGTCAGCAGCAGCACTCAGCTCTCGATGAGAAT	1640
QY	644	CTGATGATGAGCAGTAAGCTCAGGAGATGCGAGATGAGGCTCTGGACATGAGCTG 703	
DB	1639	CAATCTCAGCACACGACCTGAAAGGCCACTGAGCAGAGCTCTGAGATGGAGGAC	
QY	704	GRGGCTGACCCGGCGGAGAAGAGATTCGGCGAGCTGGAACAGGAACTGATGAGCTG 763	
DB	1579	CTGGAGATCGTCGACAAACAGTAAATTGCGCTGCGAGAACGAGCTCTCGCGCTCG	1520
QY	764	CAGGTCTAGGAGCACATCACAGGATGAGCTCTCG -- GACTTGACACACAGACA 820	
DB	1519	GCGCTCTGGTGGATTCGGCTTATGTCGACCGCTGCTCTCCGAGTGTGACAAACAGACA	1460
QY	821	CTGGCACTGCTGGGGGGCGCAGTGTGGTACCTGATGCGCTGGCTGAGATCACCCTG	880
DB	1459	CTGGCTCTGGTGGATTCGGCTTATGTCGACCGCTGCTCTCCGAGTGTGACAAACAGACA	1460
QY	881	GCGAGGCAACCAAGATAACCAGATGATGNGACCTGCTCTGGAGGCTCCGCCCTCG	940
DB	1399	GTCGCGATGCCAGGACTGTTGTTGGACGTCGATCTGGGCTCTGGAGGACCCGCTCG	1340
QY	941	AAGATATCCGGAAACAGGTCATCACAGCTGAGAACACAGGGATTCCTCATGCC	1000
DB	1339	AAGATCTCTCCGGCAAGGAAACCTTAAGCTGGCTGCGACANTGGGATTCCTCATCC	1280
QY	1001	AATGAGGGTCGAGGCCATCTACATGGACGCCGGCTGCTCTGGCTGCTCCAAATGG	1060
DB	1279	ACGAGGAAAGGGCCATCTTATGACGGCACCTCTTGTATCCGCCAACAAAGCT	1220
QY	1061	CCCTCAGCAACAACTGTGTTGGATGCCAGCTGCGATTGCTGCTTCTPATCAC	1120
DB	1219	CCACTCTGGTACAACTCACAGTGAAATATCGCTGCGCTACCTTCTGTCAC	1160
QY	1121	CAGGACCTCATGCCCTCATGGGCTGAGGTGCCAGA 1160	
DB	1159	TACGAGCTGATCAACCCATCGCCAGGAGGCCAGA 1120	
RESULT 11			
ID	AAK79966	standard; DNA; 8204 BP.	
XX			
AC	AAK79966;		
XX			
DT	07-NOV-2001	(first entry)	
XX			
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34778.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
QY	346	GGCTGTCGCCCAGGCTGAGCAGCTCACCAGAGCTATGCGACCATCAGAGGC 405	
DB	1999	TCCAGTGTCCGCCATAGGAACCTGACCCCCAACTGTTGGAGTGGCTGAGCAAAGC 1940	

XX
 PN WO200157182-A2.
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 PD 09-AUG-2001.
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 PR 17-JAN-2001; 2001WO-US01354.
 PR 31-JAN-2000; 2000US-0179065.
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 PR 05-SEP-2000; 2000US-0229509.
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 PR 06-SEP-2000; 2000US-0230437.
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 PR 14-SEP-2000; 2000US-0232399.
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 PR 26-SEP-2000; 2000US-023584.
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 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249277.
 PR 17-NOV-2000; 2000US-0249299.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0253479.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0251997.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;
 XX DR WPI: 2001-483426/52.

XX PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

XX PT Disclosure; SEQ ID NO 34778; 301pp + Sequence listing; English.

XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 8204 BP; 1865 A; 2157 C; 2229 G; 1953 T; 0 other;

Query Match 10.3%; Score 159.4; DB 22; Length 8204;
 Best Local Similarity 99.4%; Pid: No. 3e-29;
 Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 AGGTATCCAAAGCCCCAACGACTCTGGTGCACCCAGGCCAGCCCCCTGGACTCA 131
 Db 3245 AGGTTTCCAAAGCCCCAACGACTCTGGTGCACCCAGGCCAGCCCCCTGGACTCA 3304

QY 132 CCAAGCGTGTGAAGAGAGTAACAGCCACTTCAGTGACCAAGGATCTGGCGCTGA 191
 Db 3305 CCAAGCGTGTGAAGAGAGTAACAGCCACTTCAGTGACCAAGGATCTGGCGCTGA 3364

QY 192 AGCCTGCAAATGACCTCTGCTCATTAATGCTGTTGCAG 232
 Db 3365 AGCCTGCAAGATGACCTCTGCTCATTAATGCTGTTGCAG 3405

RESULT 12

AAK85212
 ID AAK85212 standard; DNA; 8204 BP.
 XX AC AAK85212;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40024.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cyostatic; gene therapy; vaccine; metastasis; db. OS Homo sapiens.
 XX PR 17-JAN-2001; 2001WO-US01354.
 XX PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0182350.
 PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 14-AUG-2000; 2000US-0225267.
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 PR 14-AUG-2000; 2000US-0225758.
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 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
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 PR 08-SEP-2000; 2000US-0231414.
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 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
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 PR 14-SEP-2000; 2000US-0233063.
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 PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239337.
 PR 20-OCT-2000; 2000US-0240960.
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 PR 08-NOV-2000; 2000US-0244647.
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 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA,
 PT Barash SC,
 PT Ruben SM;
 DR WPI; 2001-483426/52.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis - Disclosure: SEQ ID NO 40024; 3071pp + Sequence Listing; English. XX AAK5951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

CC activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK5942 to AAK54950 and AAM82169 represents sequences used in the exemplification of the present invention. XX SQ Sequence 8204 BP; 1865 A; 2157 C; 2229 G; 1953 T; 0 other;

Query	Match	Score	DB	Length
QY	72 AGGTATCCAAAGCCCCAGCATCTCTGAGCACCCACGCCAGGCCAGCCCCCTGGACTCA	131	Db	3245 AGGTATCCAAAGCCCCAGCATCTCTGAGCACCCACGCCAGGCCAGCCCCCTGGACTCA
QY	132 CCAAGCGTGTGAGAGATTAACAGGCCTACTCAGGTGACCAAGGATCTGGCGCGCTGA	191	Db	3305 CCAAGCGTGTGAGAGATTAACAGGCCTACTCAGGTGACCAAGGATCTGGCGCGCTGA
QY	192 AGCTTGAAATGACCTCTGCTCTATAATGCTGTGTCAG	232	Db	3365 AGCCCTGAGATGACCTCTGCTCTATAATGCTGTGTCAG

RESULT 13

DB AAT23953 standard; cDNA to mRNA; 144 BP.

ID AAT23953

XX

AC AAT23953;

XX

DT 27-AUG-1996 (first entry)

XX

DE Human gene signature HUMGS05899.

DE

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

KW

OS Homo sapiens.

XN WO9514772-A1.

XX

PD 01-JUN-1995.

XX

PP 11-NOV-1994; 94WO-JP01916.

XX

PR 12-NOV-1993; 93JP-0355504.

XX

(MATS/) MATSUBARA K.

PA (OKUB/) OKUBO K.

XX

Matsubara K, Okubo K;

DR WPI; 1995-206931/27.

DR

PT Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues

XX

PS Claim 1; Page 1495; 2245pp; Japanese.

XX

CC A single-stranded DNA (or its complementary strand or the correspond.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AATI9001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.

SQ Sequence 144 BP; 34 A; 50 C; 15 G; 44 T; 1 other;

Query Match 7.8%; Score 121; DB 16; Length 144;

Best Local Similarity 91.7%; Bred. No. 2e-20;
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RESULT 14

AAK87783

ID AAK87783 standard; cDNA; 457 BP.

DE Human digestive system antigen coding sequence SEQ ID NO: 99.

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;

KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

KW digestive system disorder; Meckel's diverticulum; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200155314-A2.

PN WO200155314-A2.

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US01324.

XX

PR 31-JAN-2000; 2000US-017065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0188874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0205467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

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PR	05-JAN-2001;	2001US-0259678.									
XX	(HUMA-)	HUMAN GENOME SCI INC.									
XX	Rosen CA,	Barash SC,	Ruben SM;								
XX	DR	P-PSDB; AAM92010.									
XX	WPI:	2001-502630/55.									
CC	The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.										
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 XX
 XX
 PI (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-45728149.
 DR P-PSDB; AAU19989.
 XX
 PT Isolated nucleic acid molecule encoding a human liver related protein is used in preventing, treating or ameliorating disorders of the liver particularly cancer of the liver -
 XX
 PS Claim 1; SEQ ID NO 30; 526pp; English.
 XX
 CC Sequences AAS31681-AAS31825 represent cDNA molecules, which encode the liver associated polypeptides of the invention. Liver associated polypeptides and their associated polyynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a liver associated polyynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 Query Match 4.6%; Score 71.6; DB 22; length 457;
 Best Local Similarity 94.4%; Pred. No. 6.5e-08;
 Matches 85; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Mon Mar 31 14:01:49 2003

usb-09-744-125a-1.rng

Page 22

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Search completed: March 27, 2003, 05:40:40
Job time : 632 secs

OM nucleic - nucleic search, using sw model

Run on: March 27, 2003, 05:29:20 ; Search time 81 Seconds
 (without alignments)

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 Listing first 45 summaries

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Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 ; Patent No. 6417002

; GENERAL INFORMATION:

; APPLICANT: HORICK, Robert

; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISODES

; FILE REFERENCE: 0867/0D905

; CURRENT APPLICATION NUMBER: US/09/249, 585A

; CURRENT FILING DATE: 1999-02-11

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 2

; LENGTH: 1926

; TYPE: DNA

; ORGANISM: Epstein Barr Virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1926)

; OTHER INFORMATION: coding strand of EBNA-1 DNA

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Sequence 645, Appl

US-09-620-925-1.

Query Match 3.2%; Score 49.4; DB 4; Length 9600;
 Best Local Similarity 49.8%; Pred. No. 0.0033; Mismatches 126; Indels 0; Gaps 0;
 Matches 125; Conservative 0;

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QY 527 GCGAAGGCCCTGCAGGCCACTGCACTCATGAGCAGTATTACCTGTGGAGGACAG 586
Db 2322 GGGCAGGAGGGCGCAGGAGGAGGGCAGGAGGAGGGCAGGGCAGGGCG 2281
QY 587 ACAGTGACGCCAAAGSGACCAAGTGTGAACCTCTCTGATGCAAGGACCTG 646
Db 2382 GAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2441
QY 647 ATTGTGACAGTAAGCTCAAGGACATGGAGATGGTCTGGAACATGAGCTGTG 706
Db 2442 GAGAGGGCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2501
QY 707 GCTGACCCGCCAGAAGGAGATTCCGAGCTGGACAGGACTGATAAGTGGAG 766
Db 2502 GGGCAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2561
QY 767 GTGCTAGTGA 777
Db 2562 GAGGGCAGGA 2572

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QY 768 GGGCAGGAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 847

QY 848 GAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 907

QY 647 ATTGTGACAGTAAGCTCAAGGACATGGAGATGGTCTGGAACATGAGCTGTG 706

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Db 968 GGGCAGGAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 967

QY 767 GTGCTAGTGA 777

Db 1028 GAGGGCAGGA 1038

RESULT 7 US-07-884-811-15 Application US/07884811
 Sequence 15, Application US/07885971
 Patent No. 5316921

GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
 TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
 NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/884,811
 FILING DATE: 19930518
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33, 055
 REFERENCE/DOCKET NUMBER: 755.1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-3216
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10596 bases
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear

US-07-885-971-15

Query Match 3.2%; Score 49.4; DB 1; Length 10596;
 Best Local Similarity 49.8%; Pred. No. 0.0035; Mismatches 126; Indels 0; Gaps 0;
 Matches 125; Conservative 0;

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QY 527 GCGAAGGCCCTGCAGGCCACTGCACTCATGAGCAGTATTACCTGTGGAGGACAG 586
Db 2322 GGGCAGGAGGGCGCAGGAGGAGGGCAGGAGGAGGGCAGGGCAGGGCG 2281
QY 587 ACAGTGACGCCAAAGSGACCAAGTGTGAACCTCTCTGATGCAAGGACCTG 646
Db 2382 GAGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2441
QY 647 ATTGTGACAGTAAGCTCAAGGACATGGAGATGGTCTGGAACATGAGCTGTG 706
Db 2442 GAGAGGGCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2501
QY 707 GCTGACCCGCCAGAAGGAGATTCCGAGCTGGACAGGACTGATAAGTGGAG 766
Db 2502 GGGCAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2561
QY 767 GTGCTAGTGA 777
Db 2562 GAGGGCAGGA 2572

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Qy 587 ACAGTGGAGCCCTGCCAAAGGGGACCAAGGTGACTTCTTGAGCAGGACCTG 646
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Qy 647 ATTGATGACAGTAAGTCAGAGGACATGAGATGGCTCTGAACTGAGTGTG 706
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,783A
; FILING DATE: 13-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; NAME: Marchang, Diane L.
; FILING DATE: 18-MAY-92
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/885971
; FILING DATE: 18-MAY-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Marchang, Diane L.
; FILING DATE: 18-MAY-92
; REGISTRATION NUMBER: 35,600
; PRIORITY DOCKET NUMBER: P0755779P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-087-783A-15
; Query Match 3.2%; Score 49.4; DB 1; Length 10596;
; Best Local Similarity 40.8%; Pred. No. 0.0035; Gaps 0;
; Matches 125; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Qy 527 GCGAAGGCCCTGAGGCCACTGGACGCTATGAGCTATTACCTCTGGAGGACAG 586
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Qy 767 GCTCTAGTGG 777
Db 2562 GAGGGCAGGA 2572

RESULT 9
US-08-087-783A-15
; Sequence 15, Application US/08087783A
; Patient No. 5547856
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R.
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: pattern (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,088B
; FILING DATE: 09-FEB-1994
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 530
; APPLICATION NUMBER: 07/884811
; FILING DATE: 18-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gallegos, R. Thomas B
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: 755D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-2614
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-194-088B-15
; Query Match 3.2%; Score 49.4; DB 1; Length 10596;
; Best Local Similarity 49.8%; Pred. No. 0.0035; Gaps 0;
; Matches 125; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Qy 527 GCGAAGGCCCTGAGGCCACTGGACGCTATGAGCTATTACCTCTGGAGGACAG 586
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Db 2502 GGCAGGAGGGCAGGAGGAGGGCAGGAGGGCAGGAGGGCAGGAGGGCAG 2561
Qy 767 GCTCTAGTGG 777
Db 2562 GAGGGCAGGA 2572

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US-08-194-088B-15
; Sequence 15, Application US/08194088B
; Patent No. 550996
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: pattern (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,088B
; FILING DATE: 09-FEB-1994
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 530
; APPLICATION NUMBER: 07/884811
; FILING DATE: 18-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gallegos, R. Thomas B
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: 755D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-2614
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10596 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-194-088B-15
; Query Match 3.2%; Score 49.4; DB 1; Length 10596;
; Best Local Similarity 49.8%; Pred. No. 0.0035; Gaps 0;
; Matches 125; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Qy 527 GCGAAGGCCCTGAGGCCACTGGACGCTATGAGCTATTACCTCTGGAGGACAG 586
Db 2322 GGCAGGAGGGCAGGAGGAGGGCAGGAGGAGGGCAGGAGGGCAGGAGGGCAG 2381
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Db 2442 GAGGAGGGCAGGAGGGCAGGAGGAGGGCAGGAGGGCAGGAGGGCAGGAGGGCAG 2501

Qy 7.07 GCTGCCGCCAGAACGAGAGATTCGGCAGCTGAAACAGGAATGCAATAAGTGGAG 766
Db 2502 GGGCAGGGCAGGAGCAGGAGGAGGGCAGGGCAGGGCAGGGCAGGAGGAGGAGGAGG 2561

Qy 7.67 GTGCTAGTGA 777
Db 2562 GAGGGCAGGA 2572

RESULT 11
US-08-194-087-15
; Sequence 15, Application US/08194087
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.
; TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194, 087
FILING DATE: 1 MAY - 1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33, 055
REFERENCE/DOCKET NUMBER: 779

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear

US-08-194-087-15

Query Match 3.2%; Score 49.4; DB 2; Length 10596;
Best Local Similarity 49.8%; Pred. No. 0.0035; Mismatches 125; Conservative 0; Indels 0; Gaps 0;
Matches 125; Conservatve 0; Mismatches 126; Indels 0; Gaps 0;

Qy 527 GCGAAGGCCCTTGAGGCCACTGGCAGCTCATGAGCAGTATACCTGTGAGGACAG 586
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Qy 587 ACAGTGCAAGGCCCTCCAAAGGGACCAAGTGTGAATCTCTGATGAGGAGGACCTG 646
Db 2382 GAGGGCAGGGCAGGAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAG 2441

Qy 647 ATTGTGACGAGTAAGCTCAAGGACATGCAGATGGTCTGGACATGCTGATGGTG 706
Db 2442 GAGGGAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAG 2501

Qy 647 ATTGTGACGAGTAAGCTCAAGGACATGCAGATGGTCTGGACATGCTGATGGTG 706
Db 2442 GAGGGAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAG 2501

Qy 7.07 GCTGCCGCCAGAACGAGAGATTCGGCAGCTGAAACAGGAATGCAATAAGTGGAG 766
Db 2502 GGGCAGGGCAGGAGCAGGAGGAGGGCAGGGCAGGGCAGGGCAGGGCAGGGCAG 2561

Qy 7.67 GTGCTAGTGA 777
Db 2562 GAGGGCAGGA 2572

RESULT 13

US-08-728-323A-1

; Sequence 1, Application US/08728323A

; General Information:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzyk, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Edelman, Isidore S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA

TITLE OF INVENTION: Encoding Same And Uses Thereof

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08728-323A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

FAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3489 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..3489

; US-08-728-323A-1

Query Match 3.1%; Score 48.6; DB 2; Length 3489;
 Best Local Similarity 49.8%; Pred. No. 0.0033; Mismatches 124; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 531 AGGCCCTGAGGCCACTGGCAGCTATGAAAGCAATTACCTGCTGAGGAGGAGACAG 590
 Db 1901 AGCACAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGGATGAGCAGCAGGATG 1960

QY 591 TGCAGCCGCTGCCAACGGGCAAGTGTGACTTCCTGATGAGGAGCTGATGAGGAGCTGATG 650
 Db 1961 AGCAGCAGGAGTGGAGCAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATG 2020

QY 651 ATGACAGTHAGTCAGAGCATCGAGATGAGCTGAGCTGAGACATGAGGTGATGTTGGCTG 710
 Db 2021 AGCACAGCAGGATGAGCAGCAGGAGGATGAGCAGCAGGAGTGGAGGAGGATG 2080

QY 711 ACCGGCCAGAAGGGAGGATGGAGGATGGAGCTGAGCTGAGGAGGATGAGGAGG 770
 Db 2081 AGCAGCAGCAGGATGAGCAGGAGGATGAGCAGGAGGATGAGCAGGAGG 2140

QY 771 TAGTGA 777
 Db 2141 AGCAGGA 2147

RESULT 15
 US-08-770-3179-20/c
 ; Sequence 20, Application US/08770379
 ; General Information:
 ; Patent No. 5849564

GENERAL INFORMATION:
 APPLICANT: Chang, Yuan
 APPLICANT: Bohenzyk, Roy A.
 APPLICANT: Russo, James J.
 APPLICANT: Edelman, Isidore S.
 APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 53342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match 3.1%; Score 48.6; DB 2; Length 32207;
Best Local Similarity 49.8%; Pred. No. 0.0099; Matches 123; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY	531 AGGCCTGAGGCCACTGGAGCTATGAGAGCAGTATACCTGGAGGACAGACAG 590
Db	20096 AGCACGAGCGATGAGCAAGCAGGGATGAGCACAGCGGGATGAGCACAGGGATG 200317
QY	591 TGCACCCGCTGCCAAGGGGACCAAGCTGGTAATTCCTGTATCAGAGGACCTGATG 650
Db	20036 AGCACAGCAGGATGAGCAGGAGGATGAGCAGCAGGAGGATGAGCAGCAGGGATG 19977
QY	651 ATGACAGTAGCTCAGGACTGGAGATGGTCTGGACATAGCTGATGGGGCTG 710
Db	19976 AGCACAGCAGGATGAGCAGGAGGATGAGCACAGGGATGAGCAGCAGGGATG 19917
QY	711 ACCGGGCCAGAAGGGAGAGATCCGGCAGCTGGAGAAGGAAGCTGGATAAGTGGGGTGC 770
Db	19916 AGCACAGCAGGATGAGCAGGAGGATGAGCAGGAGGATGAGCAGGAGGAGGAGC 19857
QY	771 TAGTGA 777
Db	19856 AGCAGGA 19850

Search completed: March 27, 2003, 07:50:43
Job time : 223 secs

Run on: March 27, 2003, 07:46:17 ; Search time 186 Seconds
 (without alignments)
 7105.167 Million cell updates/sec

OM nucleic - nucleic search, using sw model

Title: US-09-744-125A-1

Perfect score: 1553

Sequence: 1 gaattcggcacgagggtgggg.....aaaaaaaactcgag 1553

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/pctodata/1/pubpna/pcr7_new_pub.seq:*

3: /cgn2_6/pctodata/1/pubpna/us06_pubcomb.seq:*

4: /cgn2_6/pctodata/1/pubpna/us07_new_pub.seq:*

5: /cgn2_6/pctodata/1/pubpna/pcrtus_pubcomb.seq:*

6: /cgn2_6/pctodata/1/pubpna/pcrtus_pubcomb.seq:*

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10: /cgn2_6/pctodata/1/pubpna/us09_pubcomb.seq:*

11: /cgn2_6/pctodata/1/pubpna/us10_new_pub.seq:*

12: /cgn2_6/pctodata/1/pubpna/us10_pubcomb.seq:*

13: /cgn2_6/pctodata/1/pubpna/us60_new_pub.seq:*

14: /cgn2_6/pctodata/1/pubpna/us60_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	214.6	13.8	371	10	US-09-783-590-2176	sequence 2176, Appl
2	157.8	10.2	318	10	US-09-783-590-10575	sequence 10575, A
3	101.2	6.5	385	10	US-09-783-590-10146	sequence 10146, A
4	71.6	4.6	457	10	US-09-764-887-30	sequence 30, Appl
5	58	3.7	2108	10	US-09-963-832-225	sequence 225, Appl
6	46.6	3.0	8459	10	US-09-817-13-8	sequence 8, Appl
7	46.6	3.0	8459	10	US-09-817-538-8	sequence 8, Appl
8	45.4	2.9	3131	10	US-09-817-913-14	sequence 14, Appl
9	45.4	2.9	3131	10	US-09-817-538-14	sequence 14, Appl
10	45.2	2.9	14800	10	US-09-954-456-1601	sequence 1601, Appl
11	43.4	2.8	7305	9	US-10-156-239-9	sequence 9, Appl
12	43.4	2.8	7305	10	US-09-793-693-9	sequence 9, Appl
13	43.4	2.8	8056	9	US-10-072-621-3	sequence 3, Appl
14	43.4	2.8	8195	9	US-10-156-239-7	sequence 7, Appl
15	43.4	2.8	8195	10	US-09-793-693-7	sequence 7, Appl
16	42.4	2.7	2553	10	US-09-815-242-7690	sequence 7690, App
17	42.2	2.7	422	9	US-09-854-133-337	Sequence 337, App
18	42.2	2.7	422	10	US-09-738-973-337	Sequence 337, App
19	2.7	765	10	US-09-925-239-143	Sequence 143, App	
20	42	2.7	1852	10	US-09-969-852-4	Sequence 4, Appl
21	42	2.7	485	9	US-09-993-598-245	Sequence 245, App
22	40.6	2.6	485	9	US-09-998-293-245	Sequence 245, App
23	40.6	2.6	485	9	US-10-063-547-43	Sequence 43, Appl
24	40.6	2.6	485	9	US-09-983-733-245	Sequence 245, App
25	40.6	2.6	485	9	US-09-990-441-245	Sequence 245, App
26	40.6	2.6	485	9	US-09-980-730-245	Sequence 245, App
27	40.6	2.6	485	9	US-09-990-436-245	Sequence 245, App
28	40.6	2.6	485	9	US-09-991-181-245	Sequence 245, App
29	40.6	2.6	485	9	US-10-175-737-185	Sequence 245, App
30	40.6	2.6	485	9	US-10-993-687-245	Sequence 245, App
31	40.6	2.6	485	9	US-10-983-734-245	Sequence 245, App
32	40.6	2.6	485	9	US-09-997-653-245	Sequence 245, App
33	40.6	2.6	485	9	US-10-174-590-185	Sequence 185, App
34	40.6	2.6	485	9	US-10-175-575-185	Sequence 185, App
35	40.6	2.6	485	9	US-10-165-616-43	Sequence 185, App
36	40.6	2.6	485	9	US-10-175-737-185	Sequence 185, App
37	40.6	2.6	485	9	US-10-993-667-245	Sequence 185, App
38	40.6	2.6	485	9	US-10-063-503-43	Sequence 43, Appl
39	40.6	2.6	485	9	US-10-173-706-185	Sequence 185, App
40	40.6	2.6	485	9	US-10-175-752-185	Sequence 185, App
41	40.6	2.6	485	9	US-10-176-482-185	Sequence 185, App
42	40.6	2.6	485	9	US-10-176-913-185	Sequence 185, App
43	40.6	2.6	485	9	US-10-176-913-185	Sequence 185, App
44	40.6	2.6	485	9	US-10-176-913-185	Sequence 185, App
45	40.6	2.6	485	9	US-10-180-552-185	Sequence 185, App

ALIGNMENTS

RESULT 1

US-09-783-590-2176

; Sequence 2176, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Rubin, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16-2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2176
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (106)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (114)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (117)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (125)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (131)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (131)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (146)

OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (167)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (236)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (284)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (331)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (337)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (365)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (370)
 OTHER INFORMATION: n equals a,t,g, or c
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (370)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-783-590-2176

Query Match 13.8%; Score 214.6; DB 10; Length 371;
 Best Local Similarity 89.7%; Pred. No. 1.5e-55;
 Matches 314; Conservative 0; Mismatches 25; Indels 11; Gaps 8;

Qy 628 CTCCTATGCGAGGGCTGATTGAGACATAA
 Db 8 CTCCTATGCGAGGGCTGATTGAGACATAA
 Qy 688 GGAACTGAGCTGATGGTGTGCTGAGCGGCCAGAGGAGATCGGC-
 Db 68 GGAACATGAGCTGATGGTGTGCTGAGCGGCCAGAGCAGAATTTGCGTGGNA 127
 Qy 746 CAGGAAGCTGATAAGTG-GAGGTTCTAGTGAGCA
 Db 128 CAGNAACTGCTAAGTGGNCAGGCTAGTGACAGCATAGCTCCGG 187
 Qy 804 ACTTGACACACCAGCACTGCACTGCTGGCGCATGGTGGTA--
 Db 188 ACTTGACACACCAGCACTGCACTGCTGGCGCATGGTGGTA 247
 Qy 862 CTCGGTGTGAGA-TCCCCTGGCAGGACACCGA-
 Db 248 CTCGGTGTGAGAATTCTACCCCTGGCAGGACACCGAATTCACCAATTGATGTCGACCTG 919
 Qy 920 TCTCTCG-AGGGTCCGGCTGGAAAGA-TATCCCCGAAACAAAGGTGTCAT 966
 Db 308 TCTCTGGAGGGTCCGGCTGGAAAGATTCACCCNAACAGGTTCCT 357

RESULT 2
 US-09-783-590-1075
 ; Sequence 10575, Application US/09783590
 ; Patent No. US20020110850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Patrick J.
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Li, Haodong
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 ; FILE REFERENCE: PO-16-2C1
 ; CURRENT APPLICATION NUMBER: US/09-783-590
 ; CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 08/420, 856
 PRIOR FILING DATE: 1995-04-12
 PRIOR APPLICATION NUMBER: 08/346, 731
 PRIOR FILING DATE: 1994-11-21
 NUMBER OF SEQ ID NOS: 1285
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 10575
 LENGTH: 318
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (100)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (108)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (143)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (137)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (139)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (1363)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (1365)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (1370)
 OTHER INFORMATION: n equals a,t,g, or c
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (1370)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-783-590-1075

Query Match 10.2%; Score 157.8; DB 10; Length 318;
 Best Local Similarity 92.8%; Pred. No. 3.4e-38;
 Matches 192; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Qy 15 GTGGGGTGTGAGACCCGGCTGTTGGCGAGTGA
 Db 112 GTGGGGTGTGAGACCCGGCTGTTGGGGAGTGACCCCTTCAGTGA
 Qy 74 GATATCCAAGCCCCAGCACTCTGGCACCCAGGCCCTGACTAAC
 Db 172 GATATCCAAGCCCCAGCACTCTGGCACCCAGCCCTGGACTAAC
 Qy 134 AAGCCTGTG-AAGAGAGATAACGCCACTTCAAGTG-AACCAAGATCTGGCGCTGGA 191
 Db 232 AGCGTGTGAGAAGANGNANACGCCATTCAAGTGACCCAGGATCTGGGNCTGGA 291
 Qy 192 AGCCPAGAAATGACTCCTCTGTCTCAA 218
 Db 292 AGCTGAGATGACCTCTGTCTAA 318

RESULT 3
 Sequence 30, Application US/03764887
 Patent No. US20020042096A1
 GENERAL INFORMATION:
 APPLICANT: Dillon, Patrick J.
 APPLICANT: Haseltine, William A.
 APPLICANT: Li, Haodong
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
 FILE REFERENCE: PO-16.2C1
 CURRENT APPLICATION NUMBER: US/09/783,590
 CURRENT FILING DATE: 2000-02-15
 PRIOR APPLICATION NUMBER: 08/420,856
 PRIOR FILING DATE: 1995-04-12
 PRIOR APPLICATION NUMBER: 08/346,731
 PRIOR FILING DATE: 1994-11-21
 NUMBER OF SEQ ID NOS: 12485
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 10146
 LENGTH: 385
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (102)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (237)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (309)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (340)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (352)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (367)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (379)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (384)
 OTHER INFORMATION: n equals a,t,g, or c
 NAME/KEY: misc feature
 LOCATION: (385)
 OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-783-590-10146
 Query Match 6.5%; Score 101.2; DB 10; Length 385;
 Best Local Similarity 95.1%; Pred. No. 7.9e-21; Mismatches 4; Indels 3; Gaps 3;
 Matches 136; Conservative 0;
 Query 15 GGGGGTGGAAACCGGCGCTGTGGGGAGTGAACCCCTCTCGATG-AGAAAAAGAG 73
 Db 189 GTGGGGTGGAAACCGGCGCTGTGGGGAGTGAACCCCTCTCGATG-AGAAAAAGAG 248
 Qy 74 GTATCCAAMGCCCGAACAC-TCTGTGCAACCGAGCCAGGCCAGGCCCTCTGAC-C-TCA 131
 Db 249 GTATCCAAMGCCCGAACACTTCTGTGCACCGCCAGCCAGCCCTTGACTCA 308
 Qy 132 CCAGGCTGTGAAAGAGCTAA 154
 Db 309 NCAGAGCTGTGAAAGAGCTAA 331
 ; US-09-783-590-10146
 Query Match 6.5%; Score 101.2; DB 10; Length 385;
 Best Local Similarity 95.1%; Pred. No. 7.9e-21; Mismatches 4; Indels 3; Gaps 3;
 Matches 136; Conservative 0;
 Query Match 3.7%; Score 59; DB 10; Length 2108;
 Best Local Similarity 53.0%; Pred. No. 3.3e-07; Mismatches 110; Indels 0; Gaps 0;
 Matches 124; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
 Query 536 CTGGAGGCCACCTGGAGCTCATGAAAGGATTACCTGTGGAGGACAGCATGAG 595
 Db 1056 CTGAGACCTGAGCAGCAGGAGGGCAGCTGAGCACCTGGAGCAGGGCAG 1115
 Qy 596 CGCTGCCCAGGGCAACTGGTCACTGTCGATGAGGACCTGTGATGAGGAGGCTGTGATGAC 655
 Db 1116 CTGGGCTCCAGAGCAGGAGGCTGAGCTGAGAGCTGAGGAGGGCAG 1175
 Qy 656 AGTAAGCTCAAGACATCGAAATGAGSTCTGAAATGAGCTGAGTGTGCTGACCGG 715
 Db 1176 CAAAGCAGCTGGAGGAGGGGAGCTGAGCAGCTGTCGAGGGCAG 1235
 RESULT 4
 US-09-764-887-30

RESULT 6
US-09-817-913-8
Sequence 8, Application US/09817913
Patent No. US20020061860A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.15
CURRENT APPLICATION NUMBER: US/09/817,913
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 8
LENGTH: 8459
TYPE: DNA
ORGANISM: Human
US-09-817-913-8

Query Match 3.0%; Score 46.6; DB 10; Length 8459;
Best Local Similarity 49.8%; Pred. No. 0.0022; Mismatches 118; Indels 0; Gaps 0;
Matches 118; Conservative 0; MisMatches 119; Indels 0; Gaps 0;
Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 592 GCAGCCGCTGCCAAAGGGACCAAGTGTGACTCTCTGATGCCAGGACCTGTATTGA 651
Db 1080 GCACGAGGAGCTCCGGCAGCACGGCGGAGCTCCAGCAGCATCAAGATAACA 1139
Qy 652 TGACGTTAAGTCAGAGGACATGGGAGTGGAGGAGCTCTGGAACATGAGCTGATGGTGCTGA 711
Db 1140 GGAGATGTGGCATGANGACCAGCAGGAGCTGCTGGAGACACCGCGAAGCTGAGAG 1199
Qy 712 CCGGCCAGAGCAGAGATGGGAGCTGAAACGAACTCTCATTAAGTGGCAGT 768
Db 1200 GCACGCCAGGAGCTGGAGAACGACACCGGGAGCAGAGCTGAGCT 1256

RESULT 8
US-09-817-913-14
Sequence 14, Application US/09817913
Patent No. US20020061860A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION NUMBER: US/09/817,913
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 14
LENGTH: 3131
TYPE: DNA
ORGANISM: Human
US-09-817-913-14

Query Match 2.9%; Score 45.4; DB 10; Length 3131;
Best Local Similarity 51.8%; Pred. No. 0.003; Mismatches 96; Indels 0; Gaps 0;
Matches 103; Conservative 0; MisMatches 96; Indels 0; Gaps 0;

Qy 712 CCGGCCAGAGGGAGATGGGAGCTGGAACAGGAACATGCTGGAGT 771
Db 1256 GCACGCCAGGAGCTGGAGAACGACACCGGGAGCAGAGCTGAGCT 1256

RESULT 7
US-09-817-538-8
Sequence 8, Application US/09817538
Patent No. US20020137162A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.144
CURRENT APPLICATION NUMBER: US/09/817,538
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,157
PRIORITY FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 8
LENGTH: 8459
TYPE: DNA
ORGANISM: Human
US-09-817-538-8

Query Match 3.0%; Score 46.6; DB 10; Length 8459;
Best Local Similarity 49.8%; Pred. No. 0.0022; Mismatches 118; Indels 0; Gaps 0;
Matches 118; Conservative 0; MisMatches 119; Indels 0; Gaps 0;
Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 532 GGCCTGCAGGCCACATGGCAGCTCATGAGCTTAACTCTGAGGACAGCT 591
Db 1020 GGCCTCAAGCAGCAGTCAGCAGATCTCATGCCAGTTCAGAGGCA 1079
Qy 592 GCAGCCGCTGCCAAAGGGACCAAGTGTGACTCTCTGATGCCAGGACCTGTATTGA 651
Db 1080 GCACGAGGAGCTCCGGCAGCACGGCGGAGCTCCAGCAGCATCAAGATAACA 1139
Qy 652 TGACGTTAAGTCAGAGGACATGGGAGTGGAGGAGCTCTGGAACATGAGCTGATGGTGCTGA 711
Db 1140 GGAGATGTGGCATGANGACCAGCAGGAGCTGCTGGAGACACCGCGAAGCTGAGAG 1199
Qy 712 CCGGCCAGAGCAGAGATGGGAGCTGAAACGAACTCTCATTAAGTGGCAGT 768
Db 1200 GCACGCCAGGAGCTGGAGAACGACACCGGGAGCAGAGCTGAGCT 1256

RESULT 9
US-09-817-538-14
Sequence 14, Application US/09817538
Patent No. US20020137162A1
GENERAL INFORMATION:
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.144

CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIORITY APPLICATION NUMBER: US 60/192,157
; PRIORITY FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 3131
; TYPE: DNA
; ORGANISM: Human
; US-09-817-538-14

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Best Local Similarity 51.8%; Pred. No. 0.003%; Mismatches 218; Indels 3; Gaps 1;
Matches 103; Conservative 0; Mis matches 96; Indels 0; Gaps 0;

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Qy 360 TGAGGAGCTGCACCAAGAGCTATGCGCATTCAGAGCAAGGCCCTGTTAGCAAG 419
Db 7535 TGTCTGCACTCAAGTCTGAGAGATGAGCAGGGTSCAGCAGGAGCAGTCTGCAAG 7594
Qy 420 CTGAAGAGCACTGTGAGAAAGT---GGATCCACAGCCAGCCACCTGGAGACT 476
Db 7595 CGCAGGCCCCTCAGCAGAAGCTCCCTCTGAAAAGAACGAGCTGTACAGGGAGGC 7654
Qy 477 TCCAGACACCTGTGACAGACCTGTGATGCTTCTACCTGGCCGTPACCGAGGCC 536
Db 7655 TCATCTGAGCAGAGGAGGCCAGCTGGAGCTGAGCACGGAC 7714
Qy 537 TCCAGGCCACTGGCAACTCATGAGCAGTATTACCTGCTGGAGGACAGACTGGAGC 596
Db 7715 AGCAAGTGCGAGGAGCAGCCAGCAGCAGCAGAGTGGAGCAGGAACCGAGGGC 7774
Qy 597 CGCTCCCAAAGGGGACCAAGTGTGACTCTCTGATGAGGACCTGGTGGCCAGAC 656
Db 7775 TGGTGGCCAGCATGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 7834
Qy 657 GAACTCTAAGGACATGCGAGATGAGTGGTCTGAGCATGAGCTGTGCTGACGGG 716
Db 7835 GCAACGAGGAGCTGAGCTGAGCTGAGCAGCAAGGGGGGGGGGGGGGGGGGG 7894
Qy 717 GCCAGAGCGAGGAGTGGCAGCTGGAACAGGAATGCAATAAGTGGCAG 766
Db 7895 CTGAGSGAGAACGAGGAGCTGGTGTGAGCAGCTGCTCCAGGAGGACAG 7944

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RESULT 10
US-09-954-456-1601
; Sequence 1601, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; FILE REFERENCE: Setb
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1601
; LENGTH: 14800
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-456-1601

Query Match 2.9%; Score 45.2; DB 10; Length 14800;
Best Local Similarity 45.3%; Pred. No. 0.019%; Mismatches 191; Indels 0; Gaps 0;

Best Local Similarity 46.1%; Pred. No. 0.008%; Mismatches 218; Indels 3; Gaps 1;
Matches 189; Conservative 0; Mis matches 189; Indels 0; Gaps 0;

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Qy 360 TGAGGAGCTGCACCAAGAGCTATGCGCATTCAGAGCAAGGCCCTGTTAGCAAG 419
Db 7535 TGTCTGCACTCAAGTCTGAGAGATGAGCAGGGTSCAGCAGGAGCAGTCTGCAAG 7594
Qy 420 CTGAAGAGCACTGTGAGAAAGT---GGATCCACAGCCAGCCACCTGGAGACT 476
Db 7595 CGCAGGCCCCTCAGCAGAAGCTCCCTCTGAAAAGAACGAGCTGTACAGGGAGGC 7654
Qy 477 TCCAGACACCTGTGACAGACCTGTGATGCTTCTACCTGGCCGTPACCGAGGCC 536
Db 7655 TCATCTGAGCAGAGGAGGCCAGCTGGAGCTGAGCACGGAC 7714
Qy 537 TCCAGGCCACTGGCAACTCATGAGCAGTATTACCTGCTGGAGGACAGACTGGAGC 596
Db 7715 AGCAAGTGCGAGGAGCAGCCAGCAGCAGCAGAGTGGAGCAGGAACCGAGGGC 7774
Qy 597 CGCTCCCAAAGGGGACCAAGTGTGACTCTCTGATGAGGACCTGGTGGCCAGAC 656
Db 7775 TGGTGGCCAGCATGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 7834
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Db 7835 GCAACGAGGAGCTGAGCTGAGCAGCAAGGGGGGGGGGGGGGGGGGGGGGG 7894
Qy 717 GCCAGAGCGAGGAGTGGCAGCTGGAACAGGAATGCAATAAGTGGCAG 766
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RESULT 11
US-10-156-239-9
; Sequence 9, Application US/10156239
; Publication No. US2003036074A1
; GENERAL INFORMATION:
; APPLICANT: Gluckmann, Maria A.
; APPLICANT: Kapeller-Siebermann, Rosana
; TITLE OF INVENTION: No. US20030360741el Nucleic Acid Sequences Encoding Human T
; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefo
; FILE REFERENCE: 358001247645
; CURRENT APPLICATION NUMBER: US/10/156,239
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-156-239-9

Query Match 2.8%; Score 43.4; DB 9; Length 7305;
Best Local Similarity 45.3%; Pred. No. 0.019%; Mismatches 191; Indels 0; Gaps 0;

RESULT 12
US-09-795-693-9
; Sequence 9, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Gluckmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; FILE REFERENCE: 35800/20292
; CURRENT APPLICATION NUMBER: US/09/795, 693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185, 906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SBQ ID NO 9
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-795-693-9

Query Match 2.8%; Score 43.4; DB 10; Length 7305;
Best Local Similarity 45.3%; Pred. No. 0.02; DB 9; Length 8056;
Matches 158; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 803 GACTTGACACCCAGACACTGGGCTGGCGGCGCATGCGGACTCTGATGGC 862
Db 2952 CCTCTGGTGTCTGGCTGCAAACTCACAAAGGTCTACAGGAGACAGCTGGC 3021.

QY 923 CTGGAGGGTCGGCTGGAGATATCCGGAAACAGGTCTACAGCTGAAGAAC 982
Db 3022 CTGACAAGCTGAGGCCACCATGTCATCTGACGGCTGTCTCCAACTGGGT 3081

QY 983 GGTTGTTCTCATGCCATGAGGCTGAGGCCATCTACAGGATGATGTTGGCT 1042
Db 3082 GGGGGGGAAAGACCACCATGTCATGCCATCTGAGCTGAGGATGAGCTGGT 3141.

QY 1043 CTCCTGGCTCCAAATGGCCCTCGAACAACTCTGGGATGAGATGGCTGGA 1102
Db 3142 TCCGCACATCTAGGGACATCCGACGATCGCAACAGCTG 3201.

QY 1103 TTGGTCTTATACCAAGGACATGCCCCTCATGGGTGAG 1151
Db 3202 GGATGTGCCGACCATGTCCTTGACGGCTCACGGTGGAGG 3250

RESULT 13
US-10-072-621-3
; Sequence 3, Application US/10072621
; Patent No. US200216913TA1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
FILE REFERENCE: 100103.402
CURRENT APPLICATION NUMBER: US/10/072, 621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8056
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-621-3

Query Match 2.8%; Score 43.4; DB 9; Length 8056;
Best Local Similarity 45.3%; Pred. No. 0.02; DB 9; Length 8056;
Matches 158; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 803 GACTTGACACCCAGACACTGGGCTGGCGGCGCATGCGGACTCTGATGGC 862
Db 2952 CCTCTGGTGTCTGGCTGCAAACTCACAAAGGTCTACAGGAGACAGCTGGC 3021.

QY 923 CTGGAGGGTCGGCTGGAGATATCCGGAAACAGGTCTACAGCTGAAGAAC 982
Db 3022 CTGACAAGCTGAGGCCACCATGTCATCTGACGGCTGTCTCCAACTGGGT 3081

QY 983 GGTTGTTCTCATGCCATGAGGCTGAGGCCATCTACAGGATGATGTTGGCT 1042
Db 3082 GGGGGGGAAAGACCACCATGTCATGCCATCTGAGCTGAGGATGAGCTGGT 3141.

QY 1043 CTCCTGGCTCCAAATGGCCCTCGAACAACTCTGGGATGAGATGGCTGGA 1102
Db 3142 TCCGCACATCTAGGGACATCCGACGATCGCAACAGCTG 3201.

QY 1103 TTGGTCTTATACCAAGGACATGCCCCTCATGGGTGAG 1151
Db 3202 GGATGTGCCGACCATGTCCTTGACGGCTCACGGTGGAGG 3250

RESULT 14
US-10-156-239-7
Sequence 7, Application US/10156239
Publication No. US20030036074A1
GENERAL INFORMATION:
APPLICANT: Gluckmann, Maria A.
TITLE OF INVENTION: Rosana
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
FILE REFERENCE: 35800/247645
CURRENT APPLICATION NUMBER: US/10/156, 239
CURRENT FILING DATE: 2002-05-24
PRIORITY NUMBER: 09/795, 693
PRIORITY FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: 60/185, 906
PRIORITY FILING DATE: 2000-02-29
PRIORITY APPLICATION NUMBER: 09/609, 557
PRIORITY FILING DATE: 2001-03-15
PRIORITY APPLICATION NUMBER: 60/192, 018
PRIORITY FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 8195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
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; US-09-744-125a-1.rnpb
; Best Local Similarity 45.3%; Pred. No. 0.021; Matches 158; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
; Query Match 2.8%; Score 43.4; DB 9; Length 8195;
; Best Local Similarity 45.3%; Pred. No. 0.021; Matches 158; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
; Qy 803 GACTTCGACACAGACACTGGCAGTGTGCCGGCCATGTGGTACCTGATGCC 862
; Db 3033 GCATGAGAGCGGCCTTGAGGAGACCCGATGGAGGAGGCCACCCACCG 3092
; Qy 863 TCGGTGAGATACCCCTGGCGAGCACCAAGGATAACCAATTGATGTGGACCTGCT 922
; Db 3093 CCTCTGGTGTGCTGGTACACTACCAAGTGTACAAAGCTACAGGAGCTGCC 3092
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; Db 3153 CTGAAACAAGCTGAGCTGACCTCTACAGAAGACAGGAGGCCACCCACCG 3212
; Qy 983 GGTGATTCCTCATGGCAATAGGGTGTGACGCCCATCTACATCGATGGAGGGCGCTG 3152
; Db 3213 GGGGGGGCAAGAACCCACCATGTCCATCTGACGCCCTGTCCTCCAAAGCTCGGT 3272
; Qy 983 GGTGATTCCTCATGGCAATAGGGTGTGACGCCCATCTACATCGATGGAGGGCGCTG 1042
; Db 3213 GGGGGGGCAAGAACCCACCATGTCCATCTGACGCCCTGTCCTCCAAAGCTCGGT 3272
; Qy 1043 CTCTGTGGCTCCAATGGGGCTTCAAGAACACTCTGTGTGGAGATGCCGCGCTGGA 1102
; Db 3273 TCGGACCATCTGGGACCATCGGACGAGCATCGGACGGAGATGGATAGATCCGAGAACCTG 3332
; Qy 1103 TCGTCTCTTATCACCGAGACCTCATGCCCTCATCAGGGCTGAGG 1151
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; Search completed: March 27, 2003, 09:16:22

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; Sequence 7, Application US/09795693
; Patent No. US2002068710A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 2,065, 519, 17114, 23821, 33894, and
; TITLE OF INVENTION: 3,263, No. US2002068710A1 Human Transporters
; FILE REFERENCE: 3580/209292
; CURRENT APPLICATION NUMBER: US/09/795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 8195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (132)...(7442)
; US-09-744-125a-1.rnpb
; Query Match 2.8%; Score 43.4; DB 10; Length 8195;

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GenCore version 5.1.4_D5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

Om nucleic - nucleic search, using sw model
Run on: March 27, 2003, 05:28:05 ; Search time 2744 Seconds
(without alignments)

9166.032 Million cell updates/sec

Title: US-09-744-125A-1

Perfect score:

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Sequence:

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

16154066 seqs, 809743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: em_estnum:*

3: em_estin:*

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_es2:*

11: gb_htc:*

12: gb_est2:*

13: gb_est3:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

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LOCUS

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DEFINITION

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PRIMERS

EST.

VERSION

AL578441.1 GI:12942519

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 966)

AUTHORS

Li,W.B., Gruber,C., Jesse,J. and Polavay,D.

TITLE

Full-length cDNA libraries and normalization

FULL-LENGTH

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 9106 ERY codex - France

Email: segrid@genoscope.cns.fr, web : www.genoscope.cns.fr.

ALIGNMENTS

RESULT 1
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ACCESSION AL578441
VERSION AL578441.1 GI:12942519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 966)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polavay,D.
TITLE Full-length cDNA libraries and normalization
FULL-LENGTH Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 9106 ERY codex - France
Email: segrid@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1. location/Qualifiers

1. organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="CSDDK01YD01"

/clone_lib="LTI NFL006 PL2"

/tissue_type="Placenta"

/note="Vector: PCMVPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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C 2	898.4	57.8	914 9 AL578980	AL578980 AL578980
C 3	890	57.3	927 9 AL523921	AL523921 AL523921
C 4	883.6	56.9	993 9 AL575639	AL575639 AL575639
C 5	876.4	56.4	913 9 AL576040	AL576040 AL576040
C 6	872	56.1	1000 9 AL581415	AL581415 AL581415

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>

Db 126 CTGGGGCCATTGATTGAGCCTTGGAGGAGTAGGGCTTGTGAGGCCAGCA 67
Qy 1346 GAGGTGAGAACCTCAGGETTCCTAGATCCAGGCCCTCCATCTCTCTAA 1405
Db 66 GAGGTGAGAACCTCAGCTTCCCTAGATCCAGGCCCTCCCATCTCTAA 7

BASE COUNT 180 a 275 c 273 g 227 t 11 others

ORIGIN

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945;	Mismatches	10	9;	
	Indels	2;		
	Gaps	2;		
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Oy	568 TTACCTGCTGGAGGCCACCTTGAGACACTCTGCAGACACTCTGATGC 627			
Db	846 TTACCTGCTGGAGGCCACCTTGAGACACTCTGCAGACACTCTGATGC 787			
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Oy	688 GGAAGATGAGCTGAGTGGCTGACGGGSCAGAGGAGATGCGSAGCTGAGA 747			
Db	726 GGAAYWTGAGCTGTATGACGGGGCAGAGGAGATTCGGAGCTGAGA 667			
Oy	748 GGAAGCTGATGAGTGGCTGAGGAGCTGAGGAGATGAGCTCACAGGAGATGCGACT 807			
Db	666 GGAAGCTGATGAGTGGCTGAGGAGATGAGCTCACAGGAGATGCGACT 607			
Oy	808 CGACACAC-CAGACACCTGGCACTGTCTGGGGACCGATGGGGACTCTGC 866			
Db	606 CGACACACACGACACTGGCACTGTCTGGGGACCGATGGGGACTCTGC 547			
Oy	867 GTGAATATCACCTGGCAGGAAACCAAGGAATACAGATGATGAGCTGAGGAGCTG 925			
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Db	366 TGTGCTCCAAATGGGGCTCTGAGCAACACTCTGTGGAGATGCCACCTGATGC 307			
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Db	306 GTCTCTTCTAACAAAGGACCTCTGGCCCTCATGGGCTGAGGCTGAGTCACA 247			
Oy	1166 COACCTGAGGAGATGGGGAGCTCTGGCCCTCTGGCCCTTCCCCTGGCCACT 1225			
Db	246 CCACCTGAGGAGTGTGGGGAGCTCTGGCCCTCTGGCCCTTCCCCTGGCCACT 187			
Oy	1226 CCAGGCCCTTGAGCTGGGAACACTCTGGGAGCTCTGGCCCTCTGGCCACT 1285			
Db	186 CCAGGCCCTTGAGCTGGGAACACTCTGGGAGCTCTGGCCCTCTGGCCACT 127			
Oy	1286 CTGGGGCCATTGAGTTGAGCTTCTAGGGAGATGGCTGCTTGTGAAGCCAGCA 1345			

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	Gaps	1;		
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Db	914 GACAGACACCCCTGATGCCCTCTACCTGGCCCTACGGCAAGCCCTGAGGCTC 855			
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Db	794 GAGCCAACCTGAGACTCTCTGATGAGGAGACAGTGGAGCCCTGCCCCAAAGG 735			
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Db	734 ACATGGAGAGTGGAGCTCTGGACATGAGCTGAGGAGCTGAGGAGCTGAGGAG 675			
Oy	729 AGATTGGGGCTGAGAACAGGAGACTGATGAGTGGAGCTGAGGAGCTGAGGAG 788			

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 cloned into the Not I and Eco RV sites of the pcmvsporT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang, Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : filiang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

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 Db 614 GATGAGCTCTCGGACTTCGACAACAGACACTGCGAGCTGCTGCAGGGCCCATGGTC 555
 Qy 849 GGTACTCTGATGCCCTCGGTGAGATCACCTGGAGCAGGACAGCAACGATACCGATG 908
 Db 554 GGTACTCTGATGCCCTCGGTGAGATCACCTGGAGCAGGACAGCAACGATACCGATG 495
 Qy 909 ATGGTGAACCTGTCCTGGAGGGCGCTGGAGATACTCCGGAAACAGGTGTCATCA 968
 Db 494 ATCTGACACTGTCCTGAGGAGTCGGCTGAGGATTCCTACATCG 435
 Qy 969 AGCTGAGAACACAGGTTCTGAGGAGTCGGCTGAGGATTCCTACATCG 1028
 Db 434 AGCTGAGAACACAGGTTCTGAGGAGTCGGCTGAGGATTCCTACATCG 375
 Qy 1029 ATGGAGACGGGCTGTCCTGGGCTCAATGGGCTCTAGCACACACTGCGTGGAGA 1088
 Db 374 ATGGAGACGGGCTGTCCTGGGCTCAATGGGCTCTAGCACACACTGCGTGGAGA 315
 Qy 1089 TCGCCAGCTGCGATTGCTCTTATCACCAAGGACCTCATGCCCTCATGGGTG 1148
 Db 314 TCGCCAGCTGCGATTGCTCTTATCACCAAGGACCTCATGCCCTCATGGGTG 255
 Qy 1149 AGGCTGCCAGATCACACACAGTGGAGATGGCTGGAGACTCGTGGAGCTGGAGA 1208
 Db 254 AGGCTGCCAGATCACACACAGTGGAGCTGGAGAGCTCGTGGAGCTGGAGA 195
 Qy 1209 CTTGTTCCCTGCACTCAGGCCCTTGAGCTGGAGACTCGTGGAGCTGGAGA 1268
 Db 194 CTGTTTCCCTGCACTCAGGCCCTTGAGCTGGAGACTCGTGGAGCTGGAGA 135
 Qy 1269 GGAGTGGAGGCTGAAGTGGGGCCATGATTGAGCTTGGAGGGATAGGCTGG 1328
 Db 134 GGAGTGGAGGCTGAAGTGGGGCCATGATTGAGCTTGGAGGGATAGGCTGG 75
 Qy 1329 CCTTGTGAGGCCAGAGGCTGAGAACCTCAGGTTCTGAGATCCAGAGCCCCTCC 1388
 Db 74 CCTTGTGAGGCCAGAGGCTGAGAACCTCAGGTTCTGAGATCCAGAGCCCCTCC 15
 Qy 1389 CATCTCTCTCTC 1402
 Db 14 MATCTCTCTC 1
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 DEFINITION AL523921 LTI_NFL003 NBC3 Homo sapiens cDNA clone CS0DC003YA08 5
 PRIME mRNA sequence.
 ACCESSION AL523921
 VERSION AL523921.1 GI:1278714
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Buttheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 927)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 FEATURES source
 Email: segref@genoscope.cnrs.fr, Web : www.genoscope.cnrs.fr.
 Location/Qualifiers 1.. 927
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DC003YA08"
 /clone_lib="LTI_NFL003_NBC3"
 BASE COUNT 216 a 261 c 268 g 169 t 13 others
 ORIGIN http://fulllength.invitrogen.com/
 Query Match 57.3%; Score 890; DB 9; Length 927;
 Matches 901; Conservative 13; Mismatches 13; Indels 1; Gaps 1;
 DB 1 TAGGTGACCAAGATCTGGCGCTGTGGAGACTCGTGGAGA 60
 Qy 223 TGTGTTGACAGAACGACTGACTCGTGGAGACTCGTGGAGA 282
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 Qy 283 CACCTTGAGGAGTCCAGGAGGGTGTGAGCTGACCCCTGCTAAGATCTGTGATCTCAA 342
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 Qy 343 GTGGCCCTGTGAGGCCATGAGGAGCTGACCCAGAGGCTATGAGGACCATCAGAGCA 402
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 Qy 403 GGCCTCTGTTAACGAGCTGAGGAGCGCTGTGAGGAGCTGACCCAGGCCAGCC 462
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 Db 300 CACCTTGAGGACCTCCAGGAGCTGTCAGACAGAACCCCTGATGCTCTACTGGCCG 359
 Qy 523 TACCGCAGGGCCCTGAGGCCACTGCGAGCTGAGCTCATGAGCTTACTCTGGAGA 582
 Db 360 TACCGCAGGGCCCTGAGGCCACTGCGAGCTGAGCTCATGAGCTTACTCTGGAGA 419
 Db 583 CACAGACAGTGGCCAGCGCTGCCAACGGGACCAAGGGACAGCTGCTGAGCTCTGTGAGCAGGAGA 642
 Db 420 CCAGACAGTGGCCAGCGCTGCCAACGGGACCAAGGGACAGCTGCTGAGCTCTGTGAGCAGGAGA 479
 Qy 643 CTGATTGATGAGAGTGAAGTCAAGGATGAGCTAGGAGATGAGGAGTGTGGAACTATGAGCTGAT 702
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 Qy 703 GGTGGCTGACCCGCCGCGAGACAGGAGATTCGGACACTGGAGACAGGAGCTCTGAGA 762
 Db 540 GGTGGCTGACCCGCCGCGAGACAGGAGATTCGGACACTGGAGACAGGAGCTCTGAGA 599
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RESULT 4

AL575639/c AL575639 AL575639 LTI NFL006 PL2 Homo sapiens mRNA linear EST 16-FEB-2001

LOCUS AL575639 prime mRNA sequence.

DEFINITION Al575639

ACCESSION Al575639

VERSION 1090

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seref@genoscope.cns.fr.

FEATURES

Source

Location/Qualifiers

1. 993 /organism="Homo sapiens"

/db_xref="NCBI_Taxon:9606"

/clone="CS0D169YL09"

/tissue="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen, 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT

206 a 276 c 285 g 220 t 6 others

ORIGIN

Query Match 56.9% Score 883.6; DB 9; Length 993; Best Local Similarity 96.1%; Pid: No. 6, 6-155; Matches 971; Conservative 4; Mismatches 14; Indels 21; Gaps 6;

Qy 488 CTGCGACAGACCTGTGCTTCACGCCGTTACCGGAAAGGCCCTGCAGCCAC 547

Db 990 CTGCGACAMAACCCCGATCCTCACT-GCCCTAACCGGAAG-CCTGCAGGCCAC 933

Qy 548 TGGCACTCTGAGAGATTACCTGTGCTGGAGGACAGTCAGCGCTGCCAA 607

Db 932 TGGCGCTCATGAGCAGTAATCCGTGAGGACAGA-----CAGCGCTGCCAA 878

Qy 608 GGGGAACTGCTGCTGCTGACTCTCTGAGGAGGCTGTGAGGACAGTCAGA 667

Db 877 -GGGACCAAGTGCTGACTCTCTGAGGACAGTCAGA 819

Qy 668 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGAGGA 727

Db 818 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGAGGA 759

BASE COUNT

728 GAGATTCGGCAGCTGGAAACAGGAACATGCATAAGTGCGAGGTGCTGTGGACAGCATCAC 787

ORIGIN

RESULT 5

AL576040/c AL576040 AL576040 LTI NFL006 PL2 Homo sapiens mRNA linear EST 16-FEB-2001

LOCUS AL576040 prime mRNA sequence.

DEFINITION Al576040

ACCESSION Al576040

VERSION 1090

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seref@genoscope.cns.fr.

FEATURES

Source

Location/Qualifiers

1. 933 /organism="Homo sapiens"

/db_xref="NCBI_Taxon:9606"

/clone="CS0D169YL09"

/tissue="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen, 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT

206 a 276 c 285 g 220 t 6 others

ORIGIN

Query Match 56.9% Score 883.6; DB 9; Length 993; Best Local Similarity 96.1%; Pid: No. 6, 6-155; Matches 971; Conservative 4; Mismatches 14; Indels 21; Gaps 6;

Qy 488 CTGCGACAGACCTGTGCTTCACGCCGTTACCGGAAAGGCCCTGCAGCCAC 547

Db 990 CTGCGACAMAACCCCGATCCTCACT-GCCCTAACCGGAAG-CCTGCAGGCCAC 933

Qy 548 TGGCACTCTGAGAGATTACCTGTGCTGGAGGACAGTCAGCGCTGCCAA 607

Db 932 TGGCGCTCATGAGCAGTAATCCGTGAGGACAGA-----CAGCGCTGCCAA 878

Qy 608 GGGGAACTGCTGCTGACTCTCTGAGGAGGCTGTGAGGACAGTCAGA 667

Db 877 -GGGACCAAGTGCTGACTCTCTGAGGACAGTCAGA 819

Qy 668 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGA 727

Db 818 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGA 759

BASE COUNT

728 GAGATTCGGCAGCTGGAAACAGGAACATGCATAAGTGCGAGGTGCTGTGGACAGCATCAC 787

ORIGIN

RESULT 5

AL576040/c AL576040 AL576040 LTI NFL006 PL2 Homo sapiens mRNA linear EST 16-FEB-2001

LOCUS AL576040 prime mRNA sequence.

DEFINITION Al576040

ACCESSION Al576040

VERSION 1090

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B.; Gruber, C.; Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seref@genoscope.cns.fr.

FEATURES

Source

Location/Qualifiers

1. 933 /organism="Homo sapiens"

/db_xref="NCBI_Taxon:9606"

/clone="CS0D169YL09"

/tissue="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen, 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT

206 a 276 c 285 g 220 t 6 others

ORIGIN

Query Match 56.9% Score 883.6; DB 9; Length 993; Best Local Similarity 96.1%; Pid: No. 6, 6-155; Matches 971; Conservative 4; Mismatches 14; Indels 21; Gaps 6;

Qy 488 CTGCGACAGACCTGTGCTTCACGCCGTTACCGGAAAGGCCCTGCAGCCAC 547

Db 990 CTGCGACAMAACCCCGATCCTCACT-GCCCTAACCGGAAG-CCTGCAGGCCAC 933

Qy 548 TGGCACTCTGAGAGATTACCTGTGCTGGAGGACAGTCAGCGCTGCCAA 607

Db 932 TGGCGCTCATGAGCAGTAATCCGTGAGGACAGA-----CAGCGCTGCCAA 878

Qy 608 GGGGAACTGCTGCTGACTCTCTGAGGAGGCTGTGAGGACAGTCAGA 667

Db 877 -GGGACCAAGTGCTGACTCTCTGAGGACAGTCAGA 819

Qy 668 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGA 727

Db 818 GACATCGAGATGAGCTCTGAGGAGGCTGTGAGGAGGCTGAGGAGGAGGA 759

BASE COUNT

728 GAGATTCGGCAGCTGGAAACAGGAACATGCATAAGTGCGAGGTGCTGTGGACAGCATCAC 787

ORIGIN

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BASE COUNT	190 a 257 c 260 g 205 t 1 others
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Query Match	56.4%; Score 876.4; DB 9; Length 913;
Best Local Similarity	98.3%; Pred. No. 1.5e-153;
Matches	910; Conservative 1; Mismatches 2; Indels 13; Gaps 2;
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Db	913 TATTACCTCTGGAGGACCGACAGCTGGCAGCCAA-GGGACCAAGTGTGAC 855
QY	626 TTCTCTGATGGAGGACCTGATGATGAGCAGTGACTGAGAATGGAGATGGTC 685
Db	854 TTCTCTGATGGAGGACCTGATGAGCAGTGACTGAGAATGGAGATGGTC 795
QY	686 CTGGACATGAGCTGATGGTGGCTGACCGGGCGAGAGATGGCACCTGGA 745
Db	794 CTGGACATGAGCTGATGGTGGCTGACCGGGCGAGAGATGGCACCTGGA 735
QY	746 CAGGAACTGATGAGGAGGTGATGGACAGCATCACAGCATGGCTCTGGAC 805
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QY	805 TTGCACAAACGAACTGGCAGTGCTGCGGGCATGTGGTACCTGCGCTCG 865
Db	674 TTGCACAAACGAACTGGCAGTGCTGCGGGCATGTGGTACCTGCGCTCG 615
QY	866 CGTGAGATCACCTGGAGAGAACAAAGATAACAGATGATGATGGACCTCTCG 925
Db	614 CGTGAGATCACCTGGAGAGAACAAAGATAACAGATGATGATGGACCTCTCG 585
QY	926 GASGGTCCGGCTGGAGAATATCCGGAAACAAGSTGTATCAAGTGAAGAACGCT 985
Db	554 GAGGTCTCGCCGCTGGAGATATCCGGAAACAAGGTGTATCAAGTGAAGAACGCT 495
QY	986 GATTTCATGCGAATGGGGCGGCCATCTACATGATGGAGGCCGGGGCTC 1045
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BASE COUNT	218 a 278 c 282 g 214 t 8 others
ORIGIN	
Query Match	56.1%; Score 872; DB 9; Length 1000;
Best Local Similarity	94.1%; Pred. No. 9.5e-153;
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QY	1166 CCACGTGAGGAATGTCGAGGAGCTGGGGCTCTGGCTGTTCCTCCACT 1225
Db	314 CCACGTGAGGAATGTCGAGGAGCTGGGGCTCTGGCTGTTCCTCCACT 255
QY	1046 TGTGGCTCCAAATGGGGCTCAAGAACAACTCTGGTGGAGATGGCCAGCTGGATC 1105
Db	434 TGTGGCTCCAAATGGGGCTCAAGAACAACTCTGGTGGAGATGGCCAGCTGGATC 375
QY	500 CTGATGCTTCTACCTGGCCCTACCGGAAGGCCCTGGAGCTGGAGCTCG 559
Db	990 CCTTRGCTCTTACCGCCCTTACCGGAAGGCCCTGGAGCTCG 934
QY	560 AAGGATTAATCTGGAGGACCGACAGTGAGCGCTGCTGCCAAAGGGACCACTG 619
Db	933 AAGGATTAATCTGGAGGACCGACAGTGAGCGCTGCTGCCAAAGGGACCACTG 874
QY	1226 CCAGGCCCTTGAGGAGACTCGGCTCTGGAAACCTGGCAGTGGAGCTCG 1285
Db	254 CCAGGCCCTTGAGGAGACTCGGCTCTGGAAACCTGGCAGTGGAGCTCG 195
QY	1286 CTGGGGCCATTGATTTGAGGAGGAGAGCTGGCTTCTGGAGGCCAGAAGCAGAGATTCGGCAG 1345
QY	680 GAGSTCTCTGACATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGAT 739

Db 813 GAGGCTCTGGACAGAGCTGATGTTGGCTGACCGCCGAGAAGGAGATGGCAG 754
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 Db 693 CGGGACTTCACACAGACACTGGAGCTCTGGGGCGCATGTGGCTACTGATG 634
 Qy 860 CGCTCGCTGAGATAACCTGGCGAGAACAGGATAACCAATTGAGCTGAGGCTG 919
 Db 633 CGCTCGCTGAGATAACCTGGCGAGAACAGGATAACCAATTGAGCTGAGGCTG 574
 Qy 920 TCTCTGGAGGTCCGCCCTGGAAAGTATCCGGAAACAGGTGATCACTGAGAAGC 979
 Db 573 TCTCTGGAGGTCCGCCCTGGAAAGTATCCGGAAACAGGTGATCACTGAGAAGC 514
 Qy 980 AACGCTGATTCTTCAATGGCAATORGGGTGACGCCCTCATACATCGTGGAGGCC 1039
 Db 513 AACGGTGATTCTTCAATGGCAATORGGGTGACGCCCTCATACATCGTGGAGGCC 454

FEATURES source
 /organism="homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="L1_NFL03_NBC3"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang, Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

Qy 1040 GTGCTCTGCTGCTCAAATGGCGCTCAGAACACTCTCTGGAGATGCCAGCTG 1099
 Db 453 GTGCTCTGCTGCTCAAATGGCGCTCAGAACACTCTCTGGAGATGCCAGCTG 394
 Qy 1100 CGATTCGTCCTCTTATCAACCGAGACTCATGGCTCATCAGGCTGAGCTCCAAG 1159
 Db 393 CGATTCGTCCTCTTATCAACCGAGACTCATGGCTCATCAGGCTGAGCTCCAAG 334
 Qy 1160 ATCACACCAGTGGGAATCTGGCTGAGACTCTGGCCCTCTCGGCCGTGTTCCCCT 1219
 Db 333 ATCACACCAGTGGGAATCTGGCTGAGACTCTGGCCCTCTCGGCCGTGTTCCCCT 274
 Qy 1220 GCACTTCAAGCCCCCTGACGACTCTGGCACTGGCTGAGCTGAGCTGGAG 1279
 Db 273 GCACTTCAAGCCCCCTGACGACTCTGGCACTGGCTGAGCTGAGCTGGAG 214
 Qy 1280 GCTGACTCTGGGGCAATTGATTGGCTGAGCTGAGCTGAGCTGAGCTGGAG 1339
 Db 213 GCTGACTCTGGGGCAATTGATTGGCTGAGCTGAGCTGAGCTGAGCTGGAG 154
 Qy 1340 CCAGCAGAGGTGAGAACCTCGAGCTCCATGAGTCAGAGCCCTCCCATCTCT 1399
 Db 153 CCAGCAGAGGTGAGAACCTCGAGCTCCATGAGTCAGAGCCCTCCCATCTCT 94
 Qy 1400 CTCTAAACACCCCTACCCCCATCTACCCCTACCTGACCTCTACTCTGGCTCTC 1459
 Db 93 CCSSCACACCCC-----CTACCCCCCTGGCTCTCTCTCTCTCTCTCTCTCT 48
 Qy 1460 CAGCTGATGCTCTGAGACTCTCTTATGGTTCTCTTGTAA 1505
 Db 47 CTGCTGATGCTCTGAGACTCTCTTGTAA 2

BASE COUNT 229 a 308 c 314 g 241 t 41 others
 ORIGIN
 Query Match 55.7%; Score 864.6; DB 9; Length 1133;
 Best Local Similarity 91.5%; Pred. No. 2.1e-151;
 Matches 930; Conservative 32; Mismatches 49; Indels 5; Gaps 5;
 Db 410 TTAGCAAAAGCTGAGGAGCTGCTGAGCAAGTGGATGACGCCACCTTG 469
 Qy 1024 TTTTAGMAAGSTGAGGAGCTGCTGAGCAAGTGGATGACGCCACCTTG 967
 Db 470 GAGACCTTCGAGACCTGTCACAGACACCCCTGATGCTTACCTGGCCCTAACCG 529
 Qy 966 AAGCTTCCGAGCC-AGTGAAGAACACCTCATGCTTCTMCCTGGCCCTAACCG 908
 Db 530 AGGCCCTCGAGGCCACTGGCACTCATGAGGAGTATTACCTGCTGGAGGACGACA 589
 Db 907 AAAGCCGGMAGGCCACTGGCSCTCTWGAGCAKATTMCCTG-TGAGGACYATMA 849
 Qy 590 GTGAGCCCTGCCCACAGGGGACCAACTGTCGAGCTGAGCTGAGGACTGATT 649
 Db 848 GAGCAGCCGCTGCCAA-GGGACCAAGGAGCAACTGTCGAGCTGAGGACTRATT 790
 Qy 650 GATGCACTGAGCTCAAGGACATCGAGATGAGTGGCTCTGAGCATGAGTGGTGGCT 709
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 Qy 710 GACCGGGCGCAAGGAGGAGATGGCAGCTGGAGCATGCTCTGGAGCATGAGTGG 769
 Db 729 MACCGGGCGMAAGGAGGAGATGGCAGCTGGAGCATGAGTGGCTCTGGAGCATGAGTGG 670
 Qy 770 CTAGTGACAGCATCACAGGCAATGGCTCTGGAGCATGCTCTGGAGCATGAGTGG 829
 Db 669 CTAGTGACAGCATCACAGGCAATGGCTCTGGAGCATGCTCTGGAGCATGAGTGG 610
 Qy 830 CTGGGGGGCGCATGGTGGGACTCTGGAGCTCTGGAGGTCGGCTGGAGATTC 889
 Db 609 CTGGGGGGCGCATGGTGGGACTCTGGAGGTCGGCTGGAGATTC 550
 Qy 890 ACCAAGGATACCGAGATGGTGGGACTCTGGAGGTCGGCTGGAGATTC 949
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 Qy 950 CGGAAACAGGTCATCAGCTGAGAACACCGTGAATGGCTCAATGGCTCAG 1009
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 Qy 1010 CGAGGCCCTTCATCATGAGTCAGCTGAGGCCGCTCTGGAGGTCGGCTGGAGATTC 1069
 Db 429 CGAGGCCCTTCATCATGAGTCAGCTGAGGCCGCTCTGGAGATTC 370
 COMMENT Contact : Genoscope

RESULT⁷
 AL523920/C Locus AL523920 1133 bp mRNA linear EST 13-FEB-2001
 DEFINITION NBC3 Homo sapiens cDNA clone CSBPC003YA08 3
 LOCUS_AL523920 prime_mRNA_sequence.
 ACCESSION AL523920
 VERSION 1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1133)
 AUTHORS Li, W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization.
 JOURNAL Unpublished (2001)
 COMMENT Contact : Genoscope

QY 1070 AACACTCTGTGGAGATGCCAGCCGATCGTTTCAACAGGACCTC 1129
 Db 369 AACACTCTGTGGAGATGCCAGCCGATCGTTTCAACAGGACCTC 310

QY 1130 ATGCCCTCATCAGGGCTGAGGCTCCAAGATCACCACAGTGAGGAATGGGAGGA 1189
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QY 1190 CTGGGGGCCCCCTTCGGGCTGTGTTCCCTGCAACTCCAGCCCCCTTGAGCTGGAACTC 1249
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QY 1250 AGGCTCTGGAAACCTGGCACTGGAGGCTGAGCTGGGGCCATGATTGAGCTT 1309
 Db 18.9 AGGCTCTGGAAACCTGGCACTGGAGGCTGAGCTGGGGCCATGATTGAGCTT 130

QY 1310 TGAGGGAGTAGGGCTGGCTTGGAACCCATTAACACACCCCTAACCTT 1425
 Db 12.9 TGAGGGAGTAGGGCTGGCTGGCTTGGAACCCATTAACACACCCCTAACCTT 14

RESULT 8

AL544010 AL544010 882 bp mRNA linear EST 16-FEB-2001

LOCUS AL544010 LTR_NFL006_Pl2 Homo sapiens cDNA clone CSOD1004YM07 3

DEFINITION prime, mRNA sequence.

ACCESSION AL544010

VERSION AL544010.1 GI:12876489

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 882)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

AUTHORS Full-length cDNA libraries and normalization

TITLE JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Séquençage

BP 191 91006 EVRY cedex - France

FEATURES source

Email: segraff@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .882

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone lib="ITI_NFL006_Pl2"
 /tissue="placenta"

/note="vector: pcMSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-dGlo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 4 others

BASE COUNT 175 a 251 c 253 g 199 t

ORIGIN

Query Match 54.4%; Score 844.8; DB 9; Length 882;
 Best Local Similarity 97.6%; Pred. No. 1.2e-147;
 Matches 868; Conservative 3; Mismatches 7; Indels 11; Gaps 1;

QY 578 GAGGACAGAGCAGCTGGCTGCCAAGGAGCCAAGTGGTCAACTCTGTGATCA 637
 Db 878 GAGGACAGAGCAGCTGGCTGCCAAGGAGCCAAGTGGTCAACTCTGTGATCA 819

QY 638 GAGGACCTGATGATGAGCAGTAGCTAACGACATGGAGATGGCTGAGCTGAG 697
 Db 818 GAGGACCTGATGATGAGCAGTAGCTAACGACATGGAGATGGCTGAGCTGAG 759

QY 698 CTGATGGGCTGACCGGGCCAGAAGGAGATCGCAGCTGGAGACAGGAACTGAT 757
 Db 758 CTGATGGGCTGACCGGGCCAGAAGGAGATCGCAGCTGGAGACAGGAACTGAT 699

QY 758 AGTGGCAGGTCTAGTGACAGCATCACAGCATGAGCTCTCGGACTTCCGACAACCG 817
 Db 638 ACTGTGGCAGGTCTAGTGACAGCATCACAGCATGAGCTCTCGGACTTCCGACAACCG 579

QY 698 AGTGGCAGGTCTAGTGACAGCATCACAGCATGAGCTCTCGGACTTCCGACAACCG 639

QY 818 ACATGGGAGTGTGGCGGGCCATGTGGCTGAGCTGGCTGGAGGATGAGATGCC 877
 Db 578 CTGGGAGAGCAACAGGATACCGATGATGTGTTGAGCTGACCTCTGGAGGTCGGCC 519

QY 878 CTGGGAGAGCAACAGGATACCGATGATGTGTTGAGCTGACCTCTGGAGGTCGGCC 937
 Db 518 TGGAGATATCCGGAAAACAGGTGTCATCAAGTCACTGAGAAGAACGGTATTCTCATT 459

QY 998 GCGAATGAGGGTGACGCCCTCATCGTGTGGAGGGCGGTGCGCTGCGCTCRAA 1057
 Db 458 GCGAATGAGGGTGACGCCCTCATCGTGTGGAGGGCGGTGCGCTGCGCTCRAA 399

QY 1058 TGGGCCCTCAGGACACACTCTGGTGGAGATGCCAGGCTGGATTGTCCTCATC 1117
 Db 398 TGGGCCCTCAGGACACACTCTGGTGGAGATGCCAGGCTGGATTGTCCTCATC 339

QY 1118 ACCAGGACCTCATGCGCTCATCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1177
 Db 338 ACCAGGACCTCATGCGCTCATCGGCTGAGCTGAGCTGAGCTGAGCTGAG 279

QY 1178 ATGGTGGAGGACTCGTGGGCCTCTGGGCTGTTCCCGCCACTCCAGCCCTTG 1237
 Db 278 GTGGTGGAGGACTCGTGGGCCTCTGGGCTGTTCCCGCCACTCCAGCCCTTG 21.9

QY 1238 AGCTGGGACTCTAGGCTCTGTGAAAACCTGGCAGTGGAGGACTCTGGGGCATT 1297
 Db 218 AGCTGGGACTCTAGGCTCTGTGAAAACCTGGCAGTGGAGGACTCTGGGGCATT 159

QY 1298 GATTTGAGCTTGAGGGATAGGGCTGCTGAGACCAAGGAGCTGAGAC 1357
 Db 158 GATTTGAGCTTGAGGGATAGGGCTGCTGAGACCAAGGAGCTGAGAC 99

QY 1358 CTGAGGCTCCCTAGATCGAGGCCCTCCATCTCTCTCTCAAACACCTAC 1417
 Db 98 CTGAGGCTCCCTAGATCGAGGCCCTCCATCTCTCTCTCAAACACCTAC 42

QY 1418 CCCCATCTACCCCATGACCTTCACTCTGCTCTCAGCTGA 1466
 Db 41 -----CTACCCCCCATGCCACCTTAACTCTGCTCTCAGCTGA 1

RESULT 9

BMS49097 BMS49097 1021 bp mRNA linear EST 20-FEB-2002

LOCUS BMS49097

DEFINITION AGENCOURT_6554149 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548420

ACCESSION BMS49097

VERSION BMS49097.1 GI:18784222

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1021)
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ARCC/DCMP/PRP cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution by: Agencourt Bioscience Corporation Found through the T.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Plate: LIAM2257 row: f column: 05 High quality sequence stop: 731.
FEATURES	Location/Qualifiers
source	1. .1021 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE-5548420" /clone lib="NIH MGC 72" /tissue type="melanotic melanoma" /lab_host="DHIOB (phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies." Technologies
BASE COUNT	232 a 292 c 292 g 195 t 10 others
ORIGIN	Query Match 53.9%; Score 836.6; DB 13; Length 1021; Best Local Similarity 96.8%; Pred. No. 3.7e-146; Matches 907; Conservative 0; Mismatches 21; Indels 9; Gaps 5;
QY	151 TAACAGGCCACTTCGGTGACCAAGCATCTGGCCGCTGGAGACCTGCAATGACTCT 210
Db	1 TAACAGGCCACTTCGGTGACCAAGCATCTGGCCGCTGGAGACCTGCAATGACTCT 60
QY	211 GCTCTAAATGCTGTGTGAGACACAGACGACTCTGCTCCACCTGGCGTGAATT 270
Db	61 GCTCTAAATGCTGTGTGAGACACAGACGACTCTGCTCCACCTGGCGTGAATT 120.
QY	271 CAGCTGCCGCTTACCCCTGGAGAGCTCCAGGAGCTGTGTGAGACGCTTACGATCC 330
Db	121 CAGCTGCCGCTTACCCCTGGAGAGCTCCAGGAGCTGTGTGAGACGCTTACGATCC 180
QY	331 TGTCTCTCCAACTGGCTTCAGCCATGAGGAGCTGCCACCCAGAGCTTGCAGC 390
Db	181 TGTCTCTCCAACTGGCTTCAGCCATGAGGAGCTGCCACCCAGAGCTTGCAGC 240
QY	391 CATCCAGAGCAGGCCCTGTAGCAGGAGCTGAGCAAGTGGATC 450
Db	241 CATCCAGAGCAGGCCCTGTAGCAGGAGCTGAGCAAGTGGATC 300
QY	451 GACCGCCAGCCACCTGGAGACCTTCCAGGACCTGCTGACAGCACCCCTGAGCCT 510
Db	301 GACCGCCAGCCACCTGGAGACCTGCTGACAGCACCCCTGAGCCT 360
QY	511 CTACCTGGCCGCTACCCGAGGCCCTACAGGAGCTGGAGCTCATGAGCTTATA 570
Db	361 CTACCTGGCCGCTACCCGAGGCCCTACAGGAGCTGGAGCTCATGAGCTTATA 420
QY	571 CCTGGCTGGAGGACCAGACAGTGGAGCCCTGGAGGAGCTGGAGA 630
Db	421 CCTGGCTGGAGGACCAGACAGTGGAGCCCTGGAGGAGCTGGAGA 480
QY	631 TGATCGAGGAGCTGATGAGCAAGTCAAGGATGCGAGATGGTCTGGA 690
Db	481 TGATCGAGGAGCTGATGAGCAAGTCAAGGATGCGAGATGGTCTGGA 540
QY	691 ACATGACTGATGGTCTGACCGGCCAGAGGAGAGATCCGAGCTGGAGAGA 750
Db	541 ACATGACTGATGGTCTGACCGGCCAGAGGAGAGATCCGAGCTGGAGAGA 600
QY	751 ACTGACTAAGTGGCAGGTGCTAGTGAGACAGCATCACAGGATGAGCTCTGGAGCTTGA 810
Db	601 ACTGACTAAGTGGCAGGTGCTAGTGAGACAGCATCACAGGATGAGCTCTGGAGCTTGA 660
RESULT 10	
LOCUS	AL544052 AL544052 LIT_NFL006 PL2 Homo sapiens mRNA linear EST 16-FEB-2001
DEFINITION	AL544052 LIT_NFL006 PL2 Homo sapiens cDNA clone CSOD1004YM07 5
ACCESSION	AL544052
VERSION	AL544052.1 GI:12876531
KEYWORDS	EST
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	I (bases 1 to 848) Li, W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization. Unpublished (2001)
AUTHORS	
TITLE	Contact: Genoscope
JOURNAL	Genoscope - Centre National de Sequencage
COMMENT	Email: seqrep@genoscope.cns.fr, Web : www.genoscope.cns.fr .
FEATURES	Location/Qualifiers
source	1. .848 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSOD1004YM07" /tissue type="placenta" /note="Vector: pCMV-SPORT6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMV-SPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com "
BASE COUNT	202 a 235 c 252 g 157 t 2 others
ORIGIN	Query Match 53.6%; Score 833; DB 9; Length 848; Best Local Similarity 99.4%; Pred. No. 1.9e-145; Matches 844; Conservative 2; Mismatches 12; Indels 1; Gaps 1;
QY	333 TCATCTCCAGTTGGCTCTGACGCCATGAGGAGCTGACCCAGAGCTTATGGAGCCA 392
Db	1 TCATCTCCAGTTGGCTCTGACGCCATGAGGAGCTGACCCAGAGCTTATGGAGCCA 60
QY	393 TCCAGAGCAGGCCCTGGTAGCAGGCTGAGGAGCTGCTGAGCAAAGTGGATGCA 452
Db	61 TCCAGAGCAGGCCCTGGTAGCAGGCTGAGGAGCTGCTGAGCAAAGTGGATGCA 120

	FEATURES	Email:	secref@genoscope.cns.fr,	Web :	www.genoscope.cns.fr.
	source	Location/Qualifiers	1..947	/organism="Homo sapiens"	
Db	121 CCAGCAGCCACCTGGAGACCTTCCAGGACTCTGAGCACAGAACCTGTGCTCT	/ab_xref="taxon:9606"		/clone="CSIDC021YD221"	
Qy	513 ACTTGCGCCGTACCGCGAAGGCCCTGCAGGACCTTCAGCACAGAACCTGTGCTCT	/sex="male"		/tissue_type="neuroblastoma cells"	
Db	181 ACCTGCGCGTACCGCGAAGGCCCTGCAGGACCTTCAGCACAGAACCTGTGCTCT	/lab_host="DH10B"		/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850 USA. Fax : (1) 301 610 8371 Email : fliang@fetch.com URL : http://fulllength.invitrogen.com"	
Qy	573 TGTGAGGACAGAAGTCGACCGCTGCCAAAGGGACCAAGTGTGAATTCTCTG	240			
Db	241 TGTGAGGACAGAAGTCGACCGCTGCCAAAGGGACCAAGTGTGAATTCTCTG	300			
Qy	633 ATGGAGGACCTGATGATGACAGCTGAGCTCAGGACATGCGAGATGAGTCCTGGAC	692			
Db	301 ATGGAGGACCTGATGACAGCTGAGCTCAGGACATGCGAGATGAGTCCTGGAC	360			
Qy	693 ATGGAGGACCTGATGACAGCTGAGCTCAGGACATGCGAGATGAGTCCTGGAC	752			
Db	361 ATGGAGGACCTGATGACAGCTGAGCTCAGGACATGCGAGATGAGTCCTGGAC	420			
Qy	753 TGCATAAGTGGCGAGGTGCTAGTGCAGCATCAGGGATGACTCTCGGACTTCACA	812			
Db	421 TGCATAAGTGGCGAGGTGCTAGTGCAGCATCAGGGATGACTCTCGGACTTCACA	480			
Qy	813 ACCAGACACTGGCGATGGCTGGGGCGCATGGTACCTGATGATGCTCGTGAGA	872			
Db	481 ACCAGACACTGGCGATGGCTGGGGCGCATGGTACCTGATGCTCGTGAGA	540			
Qy	873 TCACCTCGGCAAGGAAACCAAGATTAACCAAGTTGATGTGAGCTCTGGAGTC	932			
Db	541 TCACCTCGGCAAGGAAACCAAGATTAACCAAGTTGATGTGAGCTCTGGAGTC	600			
Qy	933 CGCCCTGGAGATATCCCGAACAGGTCTCAAGTGAAGACACGGTGTACGTTCT	992			
Db	601 CGCCCTGGAGATATCCCGAACAGGTCTCAAGTGAAGACACGGTGTACGTTCT	660			
Qy	993 TCATGGCCATGAGGGTCACGGCCATCTACATGATGACGCCGGTCTGTGACT	1052			
Db	661 TCATGGCCATGAGGGTCACGGCCATCTACATGATGACGCCGGTCTGTGACT	720			
Qy	1053 CCAAATGGCGCTTCAGCAACATCTGCTGTGAGATGCCACSGCTGGATTCGTCTTC	1112			
Db	721 CCAAATGGCGCTTCAGCAACATCTGCTGTGAGATGCCACSGCTGGATTCGTCTTC	779			
Qy	1113 TTATCAACAGGACCTCATGGCCATCAGGGCTGGCTGCCAGATCACCCAGT	1172			
Db	780 TTATCAACAGGACCTCATGGCCATCAGGGCTGGCTGCCAGATCACCCAGT	839			
Qy	1173 GAGGATGG 1181				
Db	840 GAGGATGG 848				
RESULT 11					
AL527295/c	Locus AL527295	947 bp mRNA linear EST 13-FEB-2001			
DEFINITION	AL527295 LTI_NFL003 NBC3 Homo sapiens cDNA clone CS0DC021YD22 3				
PRIMERS	mRNA sequence.				
ACCESSION	AL527295				
VERSION	AL527295.1	GI:12790788			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 947)				
AUTHORS	J. W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				
	Genoscope - Centre National de Séquençage				
	BP 191 91006 EVRY cedex - France				

RESULT 12
AL529425/c AL529425 852 bp mRNA linear EST 13-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL529425
VERSION AL529425.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 852)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES source
1. 852 /organism="Homo sapiens"
/db_xref="taxon: 9606"
/clone_id="SSDD006Y005"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_hof="DHOB"
/note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
<http://fulllength.invitrogen.com>"
BASE COUNT 163 a 230 g 180 t 17 others
ORIGIN
Query Match 53.0%; Score 823.4; DB 9; Length 852;
Best Local Similarity 96.6%; Pred. No. 1.2e-143;
Matches 823; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
Db 182 CTCAGCTGGGGCATGATTTGAGCTTGAGGAGTAGGGGCCTTGAGAAGC 1340
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 916)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 13
AL571554/c AL571554 916 bp mRNA linear EST 16-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 793)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 14
TCTCTAAACAACTCTACCCCAATTCTACCTCTACTCTGTGTCT 1458
Db 62 TCTCTAAACAACTCTACCCCAATTCTACCTCTACTCTGTGTCT 14
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1398)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 15
CCAGGTGATAGC 1471
Db 13 CCAGGTGATAGC 1
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 123)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 16
TGCAGATGAGTCCTGGAGACATAGCTAGCTGATGGCTGACCGCCAGAGAGA 613
Db 672 TGCAGATGAGTCCTGGAGACATAGCTAGCTGATGGCTGACCGCCAGAGAGA 673
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 63)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 17
TGAGCTCTCGACTTCGAGACATGGCTGAGCTGGAGTGTGGGGCCATGGCGCT 851
Db 552 TGAGCTCTCGACTTCGAGACATGGCTGAGCTGGAGTGTGGGGCCATGGCGCT 493
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 373)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 18
ACCTGATGCGCTCGTGGAGACAGCTGCGAGCTGCGAGCTGCGAGTGTGGAGATCG 911
Db 492 ACCTGATGCGCTCGTGGAGACAGCTGCGAGCTGCGAGCTGCGAGTGTGGAGATCG 433
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 253)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 19
TGACCTGCTCTCTGAGGTCGCGCTGGAGATTCGGCATAGGGTCACTACATCGATG 971
Db 912 TGACCTGCTCTCTGAGGTCGCGCTGGAGATTCGGCATAGGGTCACTACATCGATG 971
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1031)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 20
TGAGGACAACTGGATTCCTATGCCAACAGGTCGAGCTGGGGCCCTCTCACATCGATG 313
Db 372 TGAGGACAACTGGATTCCTATGCCAACAGGTCGAGCTGGGGCCCTCTCACATCGATG 313
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 193)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 21
GACCGCGGCTGCTGGAGATCCAAATGGCGCTTCAGCACAACTCTGGTGGAGATCG 1091
Db 312 GACCGCGGCTGCTGGAGATCCAAATGGCGCTTCAGCACAACTCTGGTGGAGATCG 253
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 1211)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 22
CTGCCAAGATCACCAACAGCTCAGGCCCTTGAGCTGGGACTCTGGCTCTGGAA 1272
Db 192 CTGCCAAGATCACCAACAGCTCAGGCCCTTGAGCTGGGACTCTGGCTCTGGAA 1271
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 133)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 23
TTTCCCTGACGCCAGCCCCCTDAGTGGAACTCGGCTCTGAAAAGCTGGC 1272
Db 132 TTTCCCTGACGCCAGCCCCCTDAGTGGAACTCGGCTCTGAAAAGCTGGC 73
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 73)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 24
AGTGGAGGCTCAGTCGGGCCATTAGCTGAGCTTGGGGAGGATAGGGCTGGCT 13
Db 72 AGTGGAGGCTCAGTCGGGCCATTAGCTGAGCTTGGGGAGGATAGGGCTGGCT 13
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 13)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

RESULT 25
TGTGAAGCCAG 1343
Db 12 TGTGAAGCCAG 1
DEFINITION prime, mRNA sequence.
ACCESSION AL571554
VERSION AL571554.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 12)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Séquençage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES		Source
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		Location/Qualifiers
1. : ;		1. : ;
. 860		. 860
/clone lib="LTI_NFL003_NB3"		/clone lib="LTI_NFL003_NB3"
/sex="Male"		/sex="Male"
/tissue_type="neuroblastoma cells"		/tissue_type="neuroblastoma cells"
/note=organ: brain; vector: pcmsport 6; 1st strand cDNA		/note=organ: brain; vector: pcmsport 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end		enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcmsport 6		cloned into the Not I and Eco RV sites of the pcmsport 6
vector. Library was normalized. Library was constructed		vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life		Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610		8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"		http://fulllength.invitrogen.com"
8 others		8 others
BASE COUNT	a 259 c 234 g 199 t	
ORIGIN		
Query Match 52.3%; Score 812.4; DB 9; Length 860;		
Best Local Similarity 96.6%; Pred. No. 1.3e-141; Mismatches 8; Gaps 1;		
Matches 831; Conservative 8; Indels 1; Gaps 1;		
Qy 489 TGCAGACACCTGTATGCCCTCATCGCCGCTGACGGCTGCGG 1188		
356 CATGGCCYTCATCAGGGCTGAGGCTGCCAAGATCACACAGTGAGG 297		
1189 ACTGGGACCTCTGGCCCTGGCTTCCCTKFACTCCAGCCCTTGATGCTGGAC 1247		
296 ACTGGGACCTCTGGCCCTGGCTTCCCTKFACTCCAGCCCTTGATGCTGGAC 237		
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236 TCAGCTCCCTGAAAACCTGGGAGTGGCTAGTGTGGCYATNTGATGAGC 177		
1307 CTTGGAGGAGATAGGGCTGGCTTGTGAGCCAGCAGGGCTGAGACTCTAGCT 1366		
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116 CTTAKATCGAGGCCCTCSBRCTTCCTCTCTCTAAATAACACC-----C 68		
1427 TACCCCATTCGACCTTCATCTCTGCTCCAGCTGATAGCTCGAGCTTCTCT 1486		
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VERSION		
NETWORKS		
SOURCE		
ORGANISM		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE 1 (bases 1 to 860)		
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE Full-length cDNA libraries and normalization		
COMMENT Unpublished (2001)		
Contact: Genoscope		

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Qy 1269 GGCAGTGGAGGCTCACTTGCGGGCCATTGATTGASCCTTGAGGGAGGATAGG-GCTG 1327
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Db 20 GCCTTGAAACCCAAGA 1

Search completed: March 27, 2003, 07:47:14
Job time : 2780 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on:

March 27, 2003, 05:05:53 ; Search time 68 Seconds

(without alignments)

764.231 Million cell updates/sec

Title: US-09-744-125A-2

Perfect score: 1996

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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14	113.5	5.7	398	22	ABP63199	Drosophila melanog
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17	110.5	5.5	530	19	AAW49042	Human low density
18	110.5	5.5	530	22	AAW82804	Drosophila melanog
19	110.5	5.5	546	22	AAW82808	Human low density
20	110.5	5.5	1213	22	AAW40015	Human polypeptide
21	109.5	5.5	739	22	ABP62372	Drosophila melanog
22	107	5.4	557	19	AAW49039	Rabbit low density
23	107	5.4	557	22	ABP82801	Rabbit low density
24	106	5.3	519	23	AAU69430	Lung small cell ca
25	106	5.3	897	21	AAV59242	Human rod shortened dy
26	105	5.3	900	21	AAV59241	Human rod shortened dy
27	106	5.3	1092	21	AAV59237	Human rod shortened dy
28	106	5.3	1201	21	AAV59240	Human rod shortened dy
29	106	5.3	1310	21	AAV59238	Human rod shortened dy
30	106	5.3	1310	21	AAV59239	Human rod shortened dy
31	106	5.3	3685	10	AAW90373	Sequence encoded b
32	106	5.3	3685	10	AAV19838	Drosophila melanog
33	105.5	5.3	607	22	ABP61225	A rod shortened dy
34	104.5	5.2	571	21	AAV78794	A rod shortened dy
35	104.5	5.2	1219	21	AAV78795	Human antizai-2 (
36	104	5.2	367	21	AAV86211	Nuclear transport
37	103	5.2	632	20	AAV19839	B. burgdorferi ant
38	103	5.2	651	20	AAV19838	B. burgdorferi ant
39	102.5	5.1	751	22	ABP32409	Peptide #5060 enco
40	102.5	5.1	751	22	ABP37862	Peptide #5368 enco
41	102.5	5.1	751	22	ABP23121	Protein #5120 enco
42	102.5	5.1	751	22	AAW58492	Human brain expres
43	102.5	5.1	751	22	AMT0992	Human bone marrow
44	102.5	5.1	751	22	AM1164	Peptide #5069 enco
45	102.5	5.1	751	22	AAW31268	Peptide #5305 enco

ALIGNMENTS

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1995	100.0	390	21 AAY77554 Human MIF1 protein
2	1967	98.5	462	21 AAY77555 Human MIF1 protein
3	1023	51.3	578	22 ABP57874 Drosophila melanog
4	160	8.0	465	21 AAG07418 Arabidopsis thaliana
5	160	8.0	465	21 AAG0260 Arabidopsis thaliana
6	160	8.0	479	21 AAG0259 Arabidopsis thaliana
7	160	8.0	490	21 AAG07416 Arabidopsis thaliana
8	160	8.0	525	21 AAG0258 Arabidopsis thaliana
9	160	8.0	525	21 AAG0258 Human digestive sy
10	123.5	6.2	108	22 AAM92010

PT treat or diagnose, e.g. inflammation and tumors, and to identify its specific modulators, to regulate MEK kinase activity -

PT XX

XX PS Claim 20; Page 64-67; 78pp; English.

XX CC The invention provides MEK kinase (MEKK) interacting forkhead associated (MFI). MFI is useful for screening for specific modulators (potential therapeutic agents) and to reduce MEKK activity in cells. Antibodies specific to MFI are useful as diagnostic immunoassay reagents to detect expression of MFI. For purification of MFI and as therapeutic (ant)agonists. The MFI nucleic acids are useful for: recombinant production of MFI, either in cultured cells or in vivo (gene therapy); as source of probes and primers for detecting or quantifying genomic DNA encoding MFI or expression of mRNA encoding MFI; as source of therapeutic antisense sequences (used to increase MEKK activity in cells); and to identify inhibitors of MFI. Regulation of MEKK activity via MFI regulation is useful for treatment of inflammation, asthma, immunosuppression, cardiac ischemia or hypertrophy, myelodysplastic syndrome, neurodegeneration, tumours, angiogenesis, rheumatoid arthritis, psoriasis or persistent viral infections. The present sequence represents the MFI protein (plasmid pCM80).

XX SQ Sequence 390 AA;

Query Match Best Local Similarity 100.0%; Score 196; DB 21; Length 390; Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NSARGAVVERCORGSSGEPSSSEKKVSKAESTPVPVSPAPAGLTKRKVKSKQPLQVTDL 60
Db 1 NSARGAVVERCORGSSGEPSSSEKKVSKAESTPVPVSPAPAGLTKRKVKSKQPLQVTDL 60

Qy 61 GRWKANDLILNVALQTNLTSVHLGVKSCRFIREQERWMLLYPDEVISKLACQAM 120
Db 61 GRWKANDLILNVALQTNLTSVHLGVKSCRFIREQERWMLLYPDEVISKLACQAM 120

Qy 121 RQLRPEAIAAIQSKALFSKAEEQLSKGVSQSPTLETFQDQJLHRHPDAFYLTAKALQ 180
Db 121 RQLRPEAIAAIQSKALFSKAEEQLSKGVSQSPTLETFQDQJLHRHPDAFYLTAKALQ 180

Qy 181 AHWOLMKQYLLQDPTVQPLPKGDQVLFNSDAEDIDDSKLUKDKMDVELEHELMVADRQ 240
Db 181 AHWOLMKQYLLQDPTVQPLPKGDQVLFNSDAEDIDDSKLUKDKMDVELEHELMVADRQ 240

Qy 241 KREIIPQLEQFLHKQVQLVSIITGMSSPDENQTLAVLGEMWYMRMSRBTIGRATION 300
Db 241 KREIIPQLEQFLHKQVQLVSIITGMSSPDENQTLAVLGEMWYMRMSRBTIGRATION 300

Qy 301 QIDVDSLGPWKISRKGKVILKNNDDFFIANEGRPRPYIDGRPVLCGSKWRLSNNSV 360
Db 301 QIDVDSLGPWKISRKGKVILKNNDDFFIANEGRPRPYIDGRPVLCGSKWRLSNNSV 360

Qy 361 VEIASLRFVFLINQDIALTRAEEKITPQ 390
Db 361 VEIASLRFVFLINQDIALTRAEEKITPQ 390

RESULT 2

AAV7755 AAY7755 standard; Protein: 462 AA.

XX AC AAY7755;

XX DT 08-MAY-2000 (first entry)

XX DR Human MFI protein (plasmid pCM577).

XX KW MEK kinase; MEKK interacting forkhead associated protein; MFI; MEKK; FKH protein; forkhead associated protein; tumour; angiogenesis; human; psoriasis; cancer; anti-inflammatory; anti-asthmatic; immunosuppressant; vasoconstrictor; neuroprotective; antiarthritic; antiviral; Homo sapiens.

XX OS

XX WO200005362-A1.

XX PN 03-FEB-2000.

XX PD 21-JUL-1999; 99WO-EP05142.

XX DR 21-JUL-1998; 98US-0093590.

XX PA (RHON) RHONE-POULENC RORER SA.

XX PI Marcireau C, Multon M, Polard-Houset V;

XX DR WPI; 2000-195102/17.

XX N-PSDB; AAZ58958.

XX PT New MEK kinase interacting forkhead associated protein (MFI) useful to treat or diagnose, e.g. inflammation and tumors, and to identify its specific modulators, to regulate MEK kinase activity -

XX PS Claim 20; Page 70-73; 78pp; English.

XX SQ Sequence 462 AA;

Query Match Best Local Similarity 99.0%; Score 1967; DB 21; Length 462; Matches 386; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 3 ARG-GVVERCORGSSGEPSSSEKKVSKAESTPVPVSPAPAGLTKRKVKSKQPLQVTDL 60
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Qy 61 GRWKANDLILNVALQTNLTSVHLGVKSCRFIREQERWMLLYPDEVISKLACQAM 120
Db 133 GRWPADDLILNVALQTNLTSVHLGVKSCRFIREQERWMLLYPDEVISKLACQAM 192

Qy 121 RQLRPEAIAAIQSKALFSKAEEQLSKGVSQSPTLETFQDQJLHRHPDAFYLTAKALQ 180
Db 193 RQLRPEAIAAIQSKALFSKAEEQLSKGVSQSPTLETFQDQJLHRHPDAFYLTAKALQ 252

Qy 181 AHWOLMKQYLLQDPTVQPLPKGDQVLFNSDAEDIDDSKLUKDKMDVELEHELMVADRQ 240
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Qy 241 KREIIPQLEQFLHKQVQLVSIITGMSSPDENQTLAVLGEMWYMRMSRBTIGRATION 300
Db 313 KREIIPQLEQFLHKQVQLVSIITGMSSPDENQTLAVLGEMWYMRMSRBTIGRATION 372

Qy 301 QIDVDSLGPWKISRKGKVILKNNDDFFIANEGRPRPYIDGRPVLCGSKWRLSNNSV 360
Db 373 QIDVDSLGPWKISRKGKVILKNNDDFFIANEGRPRPYIDGRPVLCGSKWRLSNNSV 432

Qy 361 VEIASLRFVFLINQDIALTRAEEKITPQ 390
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PR				PR	03-AUG-1999;	9905-0147038
PR				PR	04-AUG-1999;	9905-0147204
PR				PR	04-AUG-1999;	9905-0147302
PR				PR	05-AUG-1999;	9905-0147192
PR				PR	06-AUG-1999;	9905-0147250
PR				PR	06-AUG-1999;	9905-0147303

PR	04-JUN-1999;	990US-0137502.	PR	06-AUG-1999;	990US-0147303.
PR	07-JUN-1999;	990US-0137724.	PR	06-AUG-1999;	990US-0147416.
PR	08-JUN-1999;	990US-0138094.	PR	09-AUG-1999;	990US-0147493.
PR	10-JUN-1999;	990US-0138540.	PR	09-AUG-1999;	990US-0147935.
PR	10-JUN-1999;	990US-0138847.	PR	10-AUG-1999;	990US-0148171.
PR	11-AUG-1999;	990US-0139119.	PR	11-AUG-1999;	990US-0148319.
PR	16-JUN-1999;	990US-0139452.	PR	12-AUG-1999;	990US-0148341.
PR	16-JUN-1999;	990US-0139453.	PR	13-AUG-1999;	990US-0148565.
PR	17-JUN-1999;	990US-0139459.	PR	17-AUG-1999;	990US-0148684.
PR	18-JUN-1999;	990US-0139492.	PR	16-AUG-1999;	990US-014938.
PR	18-JUN-1999;	990US-0139454.	PR	17-AUG-1999;	990US-0149175.
PR	18-JUN-1999;	990US-0139455.	PR	18-AUG-1999;	990US-0149426.
PR	18-JUN-1999;	990US-0139457.	PR	20-AUG-1999;	990US-0149722.
PR	18-JUN-1999;	990US-0139458.	PR	20-AUG-1999;	990US-0149723.
PR	18-JUN-1999;	990US-0139750.	PR	20-AUG-1999;	990US-0151065.
PR	21-JUN-1999;	990US-0139763.	PR	23-AUG-1999;	990US-0149930.
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PR	22-JUN-1999;	990US-0139899.	PR	25-AUG-1999;	990US-0150884.
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PR	24-JUN-1999;	990US-0140695.	PR	10-SEP-1999;	990US-0153070.
PR	28-JUN-1999;	990US-0140823.	PR	13-SEP-1999;	990US-0153759.
PR	29-JUN-1999;	990US-0140991.	PR	13-SEP-1999;	990US-0154018.
PR	30-JUN-1999;	990US-0141287.	PR	13-AUG-1999;	990US-0151303.
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PR	02-JUL-1999;	990US-0142055.	PR	07-SEP-1999;	990US-0152363.
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PR	08-JUL-1999;	990US-0142803.	PR	24-SEP-1999;	990US-0155659.
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PR	12-JUL-1999;	990US-0142977.	PR	16-SEP-1999;	990US-0156596.
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PR	14-JUL-1999;	990US-0143624.	PR	22-SEP-1999;	990US-0157753.
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PR	17-JUL-1999;	990US-0144086.	PR	08-OCT-1999;	990US-0158232.
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PR	19-JUL-1999;	990US-0144325.	PR	04-OCT-1999;	990US-0157117.
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PR	20-JUL-1999;	990US-0144352.	PR	14-OCT-1999;	990US-0159330.
PR	20-JUL-1999;	990US-0144632.	PR	12-OCT-1999;	990US-0159331.
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PR	21-JUL-1999;	990US-0144814.	PR	18-OCT-1999;	990US-0159584.
PR	21-JUL-1999;	990US-0145086.	PR	21-OCT-1999;	990US-0160741.
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PR	22-JUL-1999;	990US-0145276.	PR	21-OCT-1999;	990US-0161404.
PR	22-JUL-1999;	990US-01455913.	PR	21-OCT-1999;	990US-0161405.
PR	23-JUL-1999;	990US-0145145.	PR	25-OCT-1999;	990US-0161406.
PR	27-JUL-1999;	990US-0145919.	PR	22-OCT-1999;	990US-0160980.
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PR	04-AUG-1999;	990US-0147204.	PR	26-OCT-1999;	990US-0161359.
PR	04-AUG-1999;	990US-0147302.	PR	26-OCT-1999;	990US-0161360.
PR	05-AUG-1999;	990US-0147192.	PR	28-OCT-1999;	990US-0161920.
PR	05-AUG-1999;	990US-0147260.	PR	28-OCT-1999;	990US-0161993.
PR	05-AUG-1999;	990US-0147260.	PR	29-OCT-1999;	990US-0162142.

Query Match 8.0%; Score 160; DB 21; Length 479;
 Best Local Similarity 27.0%; Pred. No. 1.1e-05;

Matches	47;	Conservative	36:	Mismatches	75;	Indels	16;	Gaps	3;
QY	211	DAEIDID-DSKLU-----	DMRDEVLEHLMWADDERQKRRIQLEQELHKWQVLVDSTG	263					
PR		: : ::	: : ::						
Db	293	DGEEBIDIDAWIRKUNLVPDSDSCFNREBNMSHPHRALIGEQ-----	CTRS	343					
QY	264	MSSPFDNDTFLAVRGGRMVRVYLMRSEITGRTATEDKDQIDVDSLIEGPAWKISRQGVK	323						
PR		: : :: : : :: : : ::	: : ::						
Db	344	MQRATIMFHGAIAVILCPSDKHFRREVIGRSGSGLNVIDLGKXNGSKISRQALVK	403						
QY	324	LKNNGDFFTANEGRPPIYIDGRPVUCGSKURISNSVNEVASTRREVFLNODLI	377						
PR		: : :: : : :: : : ::	: : ::						
Db	404	LENVGCSFSKLKNLGKOHILVNGKGULDRGQIVTLLTSCSSINIRGITEVKINKEAV	457						
RESULT	7	AAG40259							
ID	AAG40259	standard; protein; 479 AA.							
XX									
AC	AAG40259;								
XX									
DT	18-OCT-2000	(first entry)							
DE	Arabidopsis thaliana protein fragment	SEQ ID NO: 49927.							
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.								
XX									
OS	Arabidopsis thaliana.								
XX									
PN	EP1033405-A2.								
XX									
PD	06-SEP-2000.								
XX									
PR	25-FEB-2000;	2000EP-0301439.							
XX									
PR	25-FEB-1999;	99US-0121825.							
PR	05-MAR-1999;	99US-0123180.							
PR	09-MAR-1999;	99US-0123548.							
PR	23-MAR-1999;	99US-0123788.							
PR	25-MAR-1999;	99US-0126264.							
PR	29-MAR-1999;	99US-0126885.							
PR	01-APR-1999;	99US-0127462.							
PR	06-APR-1999;	99US-0128234.							
PR	08-APR-1999;	99US-0128714.							
PR	16-APR-1999;	99US-0129845.							
PR	19-APR-1999;	99US-0130077.							
PR	21-APR-1999;	99US-0130449.							
PR	23-APR-1999;	99US-0130510.							
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PR	04-MAY-1999;	99US-0132484.							
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PR	06-MAY-1999;	99US-0132486.							
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PR	18-MAY-1999;	99US-0134768.							
PR	19-MAY-1999;	99US-0134941.							
PR	20-MAY-1999;	99US-013524.							
PR	21-MAY-1999;	99US-013553.							
PR	24-MAY-1999;	99US-0135629.							
PR	25-MAY-1999;	99US-0136021.							
PR	27-MAY-1999;	99US-0136392.							
PR	28-MAY-1999;	99US-0136782.							
PR	01-JUN-1999;	99US-0137222.							

	Best Local Similarity 27.0%;	Pred. No. 1.e-05;	Matches 47;	Conservative 36;	Mismatches 75;	Indels 16;	Gaps 3;
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PR	06-AUG-1999;	99US-0147303.					
PR	09-AUG-1999;	99US-0147493.					
PR	09-AUG-1999;	99US-0147935.					
PR	10-AUG-1999;	99US-0148171.					
PR	11-AUG-1999;	99US-0148319.					
PR	12-AUG-1999;	99US-0148341.					
PR	13-AUG-1999;	99US-0148565.					
PR	16-AUG-1999;	99US-0148684.					
PR	18-AUG-1999;	99US-0149175.					
PR	20-AUG-1999;	99US-0149426.					
PR	20-AUG-1999;	99US-0149722.					
PR	20-AUG-1999;	99US-0149929.					
PR	23-AUG-1999;	99US-0149902.					
PR	25-AUG-1999;	99US-0149930.					
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PR	27-AUG-1999;	99US-0151080.					
PR	30-AUG-1999;	99US-0151303.					
PR	31-AUG-1999;	99US-0151438.					
PR	01-SEP-1999;	99US-0151930.					
PR	07-SEP-1999;	99US-0152363.					
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PR	13-SEP-1999;	99US-0153758.					
PR	15-SEP-1999;	99US-0154018.					
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PR	20-SEP-1999;	99US-0154779.					
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PR	24-SEP-1999;	99US-0155486.					
PR	28-SEP-1999;	99US-0156458.					
PR	29-SEP-1999;	99US-0156596.					
PR	04-OCT-1999;	99US-0157117.					
PR	05-OCT-1999;	99US-0157753.					
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PR	12-OCT-1999;	99US-0158369.					
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PR	14-OCT-1999;	99US-0159331.					
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PR	25-OCT-1999;	99US-0161404.					
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PR	26-OCT-1999;	99US-0161359.					
PR	26-OCT-1999;	99US-0161360.					
PR	26-OCT-1999;	99US-0161361.					
PR	28-OCT-1999;	99US-0161920.					
PR	28-OCT-1999;	99US-0161993.					
PR	29-OCT-1999;	99US-0162142.					

Query Match

8.0%; Score 160; DB 21; Length 479;

PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	08-JUN-1999;	99US-0138094.	PR	06-AUG-1999;	99US-0147416.
PR	10-JUN-1999;	99US-0138340.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138347.	PR	10-AUG-1999;	99US-0147935.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139494.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149724.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149922.
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PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
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PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
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PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
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PR	06-JUL-1999;	99US-0142390.	PR	24-SEP-1999;	99US-0156559.
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PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
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PR	21-JUL-1999;	99US-0144914.	PR	18-OCT-1999;	99US-0159584.
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PR	23-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160768.
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PR	02-AUG-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
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PR	04-AUG-1999;	99US-0147032.	PR	26-OCT-1999;	99US-0161359.
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Query Match 8.0%; Score 160; DB 21; Length 490;
 Best Local Similarity 27.0%; Pred. No. 1.2e-05; Mismatches 36; Mismatches 75; Indels 16; Gaps 3;

Matches 47; Conservative 36; Mismatches 75; Indels 16; Gaps 3;

QY 211 DAEDLID-DSKLK---DMRDEVLEHLMVADRQREIREQLEHLHKWQVLVDSTG 263
 Db 304 DGSBEIDDAMIRKLNLYPDDSDSCFNRBEMNSKPHALIGEQ-----CIRTS 354
 QY 264 MSSPDFDNOTLAVERGRMVRYLMSREITLGRATKDNOIDVPLSLEGPAWKISRKGQVTK 323
 Db 355 MORAIMFHGAIAVHLCPDSKHFVVKREVIGRSGGLNDIDLGKQYNGSKLSRRQALVK 414
 QY 324 LKUNGDFFIANEGRPRPIVDGRPVLCGSKWRSLNSVNEIASLRPFELINQDLI 377
 Db 415 LENYGFSLKLNGLKHOHLVNGKLDRGQIVTLLSCSSINIRGIFTVFVKINKBEAV 468

RESULT 9

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 AC AAG40258;
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99TS-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
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 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX DR N-PSDB; AAK67783.
 XX Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases -
 XX
 PS Claim 11; SEQ ID NO 1359; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a digestive system antigen of
 CC the invention.
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 DT 06-DEC-2001 (first entry)
 XX Human liver associated polypeptide #20.
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KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
 KW chicken; sheep; immunosuppressive; antiarthritic; vasoactive;
 KW antirheumatic; antiproliferative; cytostatic; cardiotonic; neuroprotective;
 KW cerebroprotective; nootropic; antibacterial; fungicide; cancer;
 KW ophthalmological; pulmonary; gene therapy; autoimmune disease; neoplasm;
 KW hyperproliferative disorder; breast; liver; cardiovascular disorder;
 KW cerebrovascular disorder; nervous system disorder; bacterial infection;
 KW fungal infection; viral infection; ocular disorder; endocrine disorder;
 KW gastrointestinal disorder; renal disorder; respiratory disorder;
 KW wound healing; skin aging; organ transplantation; tissue regeneration;
 KW anti-infertility.

XX Homo sapiens.

XX OS

XX XX WO200155355-A1.

XX PD 02-AUG-2001.

XX XX 17-JAN-2001; 2001WO-US01351.

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PR 17-NOV-2000; 2000US-0249265.

PR 17-NOV-2000; 2000US-0249274.

PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0251016.

PR 05-DEC-2000; 2000US-0251031.

XX related polypeptides and antibodies -
 PS Claim 11; SEQ ID No 176; 181pp; English.
 XX
 CC The invention relates to 145 novel human liver antigens (ABP40831-
 CC ABP40795) and to cDNAs encoding them (ABN0036-ABN0180), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human liver antigen
 CC and host cells, antibodies against human liver antigens, and the use of
 CC polynucleotides, antibodies against human liver antigens, and the use of
 CC liver antigen polynucleotides and polypeptides in diagnosing, treating,
 CC prognosing or preventing various disorders of the liver. Such conditions
 CC include viral infections (e.g., cytomegalovirus, Epstein-Barr virus,
 CC hepatitis A virus, hepatitis B virus and hepatitis C virus), parasitic
 CC infections (e.g., Clonorchis sinensis, Echinococcus granulosus and
 CC Entamoeba histolytica), and also bacterial and fungal infections. Other
 CC disorders that may be treated include inflammatory conditions (e.g.,
 CC cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins,
 CC autoimmune diseases (e.g. Wilson's disease, primary biliary cirrhosis),
 CC neoplastic disorders (e.g., adenomas, haemangiomas and hepatocellular
 CC carcinoma), portal hypertension, or gastrointestinal disorders (e.g.,
 CC peptic ulcers, gastritis and peritonitis). Liver antigen
 CC compounds which modulate liver antigen expression or activity. The
 CC polynucleotides may further be used for gene therapy, chromosome
 CC mapping, in the identification of individuals and in forensic analysis,
 CC and the polypeptides may be used as molecular weight marker or to
 CC prepare antibodies useful in disease diagnosis, drug targeting and
 CC phenotyping. The present sequence represents a human liver antigen of
 CC the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence/
 XX SQ Sequence 108 AA:
 Query Match 6.2%; Score 123.5; DB 23; Length 108;
 Best Local Similarity 23.3%; Pred. No. 1; Mismatches 126; Indels 102; Gaps 21;
 Matches 86; Conservative 55; Mismatches 126; Indels 102; Gaps 21;
 QY 315 ISRKQGVKLKONGDFFIANEGRPP-IYIDGSPVLCGS 351
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 64 ISASTGVKLKONGDFFIANEGRPPSTMGR--VGCS 99
 CC :|||:|||:|||:|||:|||:|||:|||:|||:
 RESULT 13
 ABB63519
 ID ABB63519 standard; Protein; 2346 AA.
 AC
 XX
 DE 26-MAR-2002 (first entry)
 DT
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 17349.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PR 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers BW;
 XX
 DR N-PSDB; ABL07622.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX RS Disclosure; SEQ ID NO 17349; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABL57737-ABL72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2346 AA:
 Query Match 5.8%; Score 116; DB 22; Length 2346;
 Best Local Similarity 23.3%; Pred. No. 1; Mismatches 126; Indels 102; Gaps 21;
 Matches 86; Conservative 55; Mismatches 126; Indels 102; Gaps 21;
 QY 45 KEVKKSQKPLQVTKDGLGRWKPAANDLILNAVLQTNLTSVHLGVNKSCRFTIREVQEWRY 104
 CC :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 340 KKLQAMQELASANDL--LKQARESLESATCQLAASAA----ASRLRSDLSLTEL 391
 CC :|||:|||:|||:|||:|||:|||:
 QY 105 ANLYDPVPSKQACQARQLHPEAIKAOSKALSKABQ--LISRGSTSTPITLEFQDL 162
 CC :|||:|||:|||:|||:|||:
 Db 392 YSMYAKSEEL--EMLRCEBOL-KLQLKSLIAESESAPILEKQNSDIQKMKENSEL 447
 CC :|||:|||:
 QY 163 LIRHHPDAFY-----LARTPAKL-----OAHWOLMKQYLLEDQ----- 195
 CC :|||:|||:
 Db 448 IREHDELLIQNKCLERBLERALSTLHNQNENKKLQTHDSROVOMLIDELNCTRAGV 507
 CC :|||:|||:
 QY 196 --TVQP--LPK---GDDQVLNFDAEQLD--JSKLKMDRDEVLEHELMVADR---- 239
 CC :|||:|||:
 Db 508 KHVRIQPQTROPLTSESLISLDNLVTESSEIYLDRNTYLNMSREL--ELLEASEKNODK 565
 CC :|||:|||:
 QY 240 -----QKRETRQLEQELAKHQVQLVITGMSSPDFENOTQAVLVRGPNRY--LMSREBTT 292
 CC :|||:|||:
 Db 566 MILEQSKNHIRKLDAA--RFABLEDILQ----KNTNTVTLISCDRYKLYFAQQK 616
 CC :|||:|||:
 QY 293 LGRATKO-----HQIDVQLSLBQPA--WKSIRK-----QGVTK---LKN 326
 CC :|||:|||:
 Db 617 IGONTVQDLDSSNLEPDNSALDTS-EQDAAANFEESRKLKRVROLEQLEGEVKKYASLKE 675
 CC :|||:|||:
 QY 327 NGDFFIANE 335
 CC :|||:|||:
 Db 676 NYDYVTEK 684
 CC :|||:|||:
 RESULT 14
 ABB63199
 ID ABB63199 standard; Protein; 398 AA.
 XX
 AC ABB63199;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 16389.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 PN WO200171042-A2.

PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 XX
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07302.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 PT disclosure; SEQ ID NO 16389; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL1040-ABL16175) and the encoded proteins (ABBS737-ABBT202).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 CC
 XX
 SQ Sequence 398 AA;

Query Match 5.7%; Score 113.5; DB 22; Length 398;
 Best Local Similarity 29.2%; Pred. No. 0-13; Mismatches 34; Indels 21; Gaps 4;
 Matches 31; Conservative 20;

Oy 2 SARGGVVERGRCSSEPSSESSEKKVSKAPSTPVPPSAPAPGLTKRVRKSKQPLQVTKDQG 61
 Db 102 AMAGSAKEGGASTGKPKAS-----GNAPATP-PPP PPPPAKSAPPVAKKPRLKTFEY 154
 Qy 62 RWKPAN-----DL-----LLINAVLQTNDLTSHLGVKFRSCR 93
 Db 155 RWKPGDQDQPTQTYEVLDQCGAMVLDALIKRNEMDPFLTRRRSCR 200

RESULT 15

ABBL176A
 ID ABBL1764 standard; peptide; 510 AA.
 AC ABBL1764;
 DT 11-JAN-2002 (first entry)

XX Human LDL binding protein homologue, SEQ ID NO:2134.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; fibroblast; chemotaxis; chemokines; thrombolytic; onogenesis; proliferation; wound healing; infection; immune disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; drug screening; gene therapy; anti-inflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytoplastic; osteoprotective; vasotropic; cardiotonic; virucide; antibacterial; antifungal; vulnerary; antiluler.

XX Homo sapiens.

ABBL176A
 ID ABBL1764 standard; peptide; 510 AA.
 AC ABBL1764;
 DT 11-JAN-2002 (first entry)

XX Human LDL binding protein homologue, SEQ ID NO:2134.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; fibroblast; chemotaxis; chemokines; thrombolytic; onogenesis; proliferation; wound healing; infection; immune disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; drug screening; gene therapy; anti-inflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytoplastic; osteoprotective; vasotropic; cardiotonic; virucide; antibacterial; antifungal; vulnerary; antiluler.

XX Homo sapiens.

Query Match 5.5%; Score 110.5; DB 22; Length 510;
 Best Local Similarity 18.3%; Pred. No. 0-36; Mismatches 150; Indels 111; Gaps 16;
 Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16;

Oy 1 NSARGGVVERGRCSSEPSSESSEKKVSKAPSTPVPPSAPAPGLTKRVRKSKQPLQVTKDQG 50
 Db 102 NOGPGDGAQCPAEPDAEKSRTYVARNGHEPPVTUNGKEPKSKGDNPNTTEIROSDE 161
 Qy 51 -----KOPLOQTDLGKWPANDLILNIAVQT-NDLTSVHLGVKFRSCRFLREVOERW 103
 Db 162 VGDHRPQEKKAKGELGK-----ITLNGQTNLSTPEEKLAACKYAEHLBEHR 215

PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PR 05-FEB-2001; 2001WO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 XX
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 XX
 DR N-PSDB; ABA09008.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject - e.g. arthritis and cancer -

XX
 CS Claim 20; Page 240-241; 1963pp; English.

Sequences ABB10901-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10901-ABB109574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth factor activity, haemopoiesis regulatory activity, tissue growth activity, immunomodulatory activity, activin- or inhibin-related activities, chemotactic or chemokinetic activities, haemostatic, thrombotic or thrombolytic activities, receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis) and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

XX
 SQ Sequence 510 AA;

Query Match 5.5%; Score 110.5; DB 22; Length 510;
 Best Local Similarity 18.3%; Pred. No. 0-36; Mismatches 150; Indels 111; Gaps 16;
 Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16;

Oy 1 NSARGGVVERGRCSSEPSSESSEKKVSKAPSTPVPPSAPAPGLTKRVRKSKQPLQVTKDQG 50
 Db 102 NOGPGDGAQCPAEPDAEKSRTYVARNGHEPPVTUNGKEPKSKGDNPNTTEIROSDE 161
 Qy 51 -----KOPLOQTDLGKWPANDLILNIAVQT-NDLTSVHLGVKFRSCRFLREVOERW 103
 Db 162 VGDHRPQEKKAKGELGK-----ITLNGQTNLSTPEEKLAACKYAEHLBEHR 215

QY	104	YALLYPDVISKLACOMRLOHPEATAIOSKALFSKA-----
Db	216	NSQOKQMOKLUOKKOSOLVQE--KDHLRGEHSSKAVLRSKLESLCRELQRHNRSLKEGVQR
Qy	141	--EEQLSKUGSTSPTLETFDPLHLRRHPDAFLYRTAKALOAHQ-----LMQY 190
Db	274	AREEEERKEKVTSFHSPQFTNLNDIOLQMEHQNE----RNSKLUROENMELAERUKKLIQEY 328
Qy	191	LLEDQTVQPLPKGDQVLMFSDAEDLIDSKLKMDRDEVLEHEBLMVAADRROKREBIROLEQE
Db	329	LREEHIT-----DKVFHKHDLLQQQLVYDAKLOQQAQMELKE-----AEBRHRE----- 369
Qy	251	LHKWQVLFUDSTIGMSSPDFDNTOLAVERGRWMRYLMSREI---TGLHATKONQIDYDSL 308
Db	370	--KDFLILKEAVESORMCBLMKOOETHLKQOLALYTERKEFONTLISKSS---EVFTT 422
Qy	309	BGPWAKWLSRKOGVVKLNGDFPIANEGRPRPYIDGRPVLGCSKWLNSVNEUJSLR 368
Db	423	KQEMERKMTK--IKKLERETTMY-----RSRWESSNKAJJEMAEKT 462
Qy	369	V 369
Db	463	V 463

OM protein - protein search, using sw model

Run on: March 27, 2003, 05:18:00 ; Search time 25 Seconds

Title: US-09-744-125A-2

Perfect score: 1996

Sequence: 1 NSARGGVEPGRGSGSBPPSS.....LINQDILIALRAEAKITPQ 390

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/pctodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/pctodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/pctodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/pctodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/pctodata/1/iaa/PCUS_COMB.pep:*

6: /cgn2_6/pctodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	110.5	5.5	530	4	US-08-979-608A-8
2	107	5.4	557	4	US-08-979-608A-5
3	102	5.1	10182	4	US-08-134-001C-3159
4	100	5.0	15281	2	US-08-471-119A-2
5	99.5	5.0	1377	2	US-08-308-818-4
6	98.5	4.9	855	2	US-08-468-558-2
7	98.5	4.9	855	4	US-08-676-444-2
8	97.5	4.9	1048	4	US-08-887-534A-85
9	97	4.9	1168	1	US-08-620-717A-9
10	97	4.9	1232	4	US-08-592-054-2
11	95.5	4.8	503	4	US-08-740-223A-18
12	95.5	4.8	503	4	US-09-202-491-4
13	95.5	4.8	503	4	US-09-202-491-10
14	95.5	4.8	503	4	US-09-709-188-18
15	92	4.6	503	4	US-08-313-185-51
16	92	4.6	731	2	US-08-459-499-15
17	92	4.6	731	2	US-08-483-924-4
18	92	4.6	731	3	US-09-082-614A-51
19	92	4.6	2101	4	US-08-466-390-4
20	92	4.6	2101	1	US-08-470-950-4
21	92	4.6	2101	1	US-08-467-781-4
22	4.6	2101	1	US-08-195-487-4	
23	92	4.6	2101	2	US-08-493-924-4
24	92	4.6	2101	4	US-09-452-294-1
25	92	4.6	2101	5	PCT-US93-00160-4
26	91.5	4.6	1274	4	US-09-443-2
27	91	4.6	1167	1	US-08-485-568A-6

ALIGNMENTS

RESULT 1
US-08-979-608A-8
Sequence 8, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Law, Simon W.
Arizona, Anil A.
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis B.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-5906
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-979-608A-8
Query Match 5.5%; Score 110.5; DB 4; Length 530;

Best Local Similarity 18.3%; Pred. No. 0.063; Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16; Db 75 NQGPGEDGAGQGEPAPEDEAKSRTVARNEGEPEPTPVVIGEKERSKGDPNTEERIQSDS- 50 Qy 51 -----KQPLQVTQDGLGRWKPANDILLNAVLT-NDLTSVHLGKFSRFTLREVQEW 103 Db 135 VGDRHRRPQEKKAKGLGKE-----ITLMOTNTLSPEEKLAACKYAEELLEHR 188 Qy 104 YALIYDPIVSKLACAMROHPEAIAQKALFERA----- 140 Db 189 NSQKQMKLQLKKQSQLVQE-KDHURGENSKAVLRSKESLCRRLQRHNRSKKEGVQR 246 Qy 141 --BQQLSKVGSTSOPTLETFPODILHHPDAFYLARTAKALQAHQ-----LMQQQY 190 Db 247 AREEEBKKEVTSHQVTLNDIOLQOMEQNE----RNSKUROEMBLAERLKQLEQE 301 Qy 191 LLEDQTQVQPLPKGQDQVLFNEDDAEDIDDSKLKMDDEVLHELMADRKQKRETRQLBQE 250 Db 302 LREHH-----DKVKHKDLQOLQDVLDAKLUQAOQEMLK-----AERHORE----- 342 Qy 251 LHKWQVNLVDITGMSPDFMOTLAVLGRMLVRYMRSREI--TLAGRATKDQIDVDSL 308 Db 343 --KDFLILKEAVESQDMCELMKQOBTHKQOLALYTFEEKFEEFQNTUSKS----EVFTFE 395 Qy 309 EGPAWKISRKQGVNLKNNDFIANGRPRIVDGRPVLCGSKWLSSNNVTLASLR 368 Db 396 KOEMKMTK--IKLKEETMY-----RSRWESSIONKALLEMAEKT 435 Qy 369 V 369 Db 436 V 436

RESULT 2
US-09-979-608A-5
; Sequence 5, Application US/08979608A
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P. C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; COMPUTER: IBM Compatible
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08-979-608A
; FILING DATE: 26-No. 6355451-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 7-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,955
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

RESULT 3
US-09-134-001C-3159
Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: STC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3159
Query Match 5.1%; Score 102; DB 4; Length 10182;
Best Local Similarity 24.3%; Pred. No. 28; Mismatches 83; Conservative 60; Indels 62; Gaps 21; Matches 83; Conservatve 60; Mismatches 136; Indels 62; Gaps 21; SEO ID NO 3159
Qy 16 EPSSSEKKK---VSKAPSTPPVSPAPGLTR-VKKSQQLQVTQDGLRKWPANDILL 70

Best local similarity 23.2%, Pred. No. 78;
Matches 73; Conservative 47; Mismatches 118; Indels 76; Gaps 14;

```

Db 3424 EPLETAKNQLQANIDQKPS-----DGMTOQSVOSYERKLQQAKD-----KIN 3466
Qy 71 LINAVLQTN-DLTSHVLUKGKESCRFTLREVOERWALLYD-PVI-SKLAQCAQMRLHPE 126
Db 3467 SIIINVVLNPDVNAARTN-KVETBQINNLTOAQGLTVDKOPLNACTALOOSIDNQPS 3525
Qy 127 AI---ANQOS-KALFSKAEE--QLSKVGSTSOPTLETQFDIHLHRHPDAFYLARTAK-A 178
Db 3526 TTGTEATIOTNQYNAQRQAEQVONAMKNIENAOQPSVQVSDESKSKEQALSILNAKSA 3585
Qy 179 LOAQMWLQCYQYLLEPDTQVPL----PKGDQTFNFSDAEDLIDDSKUKMDMDEV-EH 231
Db 3586 LRADKQELQOQAY--NQLIOPTDLINKKAPASITYANQRYQOFNSNELNSTKTNTDRILKEQ 3642
Qy 232 ELMVAD-RRQKRETRQLQFELHKWQVUDSITGMSSPFEDNQTLAVLGRGRMVTYL-MRS 288
Db 3643 NPSPYADVANNALKYREVQDOKLNBARALLQD-----KEDNALSIVRAKEQLOQAOAVDQPS 3695
Qy 289 REITLGRATKDQNDVLSLEGPAWKISRKGVTLLKONGD 329
Db 3696 TE-GMTQQTKD--DYNISKQQAQEQBEISKAQQV--DNGD 3729

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RESULT 4

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US-08-471-119A-2
; Sequence 2, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Leitner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoergendorfer, Kurt
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatientIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 874
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolyphocladium niveum
; STRAIN: ATCC 34921
; US-08-471-119A-2

```

Query Match 5.0%; Score 100; DB 2; Length 15281;

Best local similarity 23.2%, Pred. No. 78;
Matches 73; Conservative 47; Mismatches 118; Indels 76; Gaps 14;

```

Qy 14 GSRSSEKKKSKAPSVPVPPAPGGLTRKVKESKQPLQVTKDQGRMKAN-DULLI 72
Db 2126 GLPSSOSVQFVNKAADF-----FPGLB--GKQVHVTAMDPGRLSLSPDILIV 2174
Qy 73 NAVLQTNDLTSVHLGVKESCRFTLREVOERWALLYDPMVSKLAQCMRQ-----LHP 125
Db 2175 NSIAQ-----YFPSREVLAEV-----ALVRIPGVRLIFGGDMRTVATHKDFLVA 2220
Qy 126 EAIAATOSKALFSKAEBOLSKVGTSOPTLETQFDIHLHRHPDAFYLARTAK-AQAHWQ 185
Db 2221 RAVHTNGSRVTRSKVQEV-----ARLBBLLEELLVNDP-AFFIS----- 2258
Qy 186 MKQYVLEDDQTPOLPKCDQVNFSDAEDLIDDSKUKMDMDEV-EH 245
Db 2259 QLEQELHKM-----QVLDSTTGMSSPFDNQTLAVLGRGRMVRMLRSRET-TUGRATKD 249
Qy 2307 KINAЕ-SWIDFASSQMDRQGLARLLENKENKODESIAVNIPKSTIV-ERHAKSLADDH 2363
Qy 300 NOIDVDSLLEGPAW 313
Db 2364 DGGDDTHSSSIDGVAM 2377

```

RESULT 5

```

US-08-453-418-2
; Sequence 2, Application US/08463418
; Patent No. 5908971
; GENERAL INFORMATION:
; APPLICANT: Van Der Straeten, Dominique et al.
; TITLE OF INVENTION: CRUCIFER ACC SYNTHASE AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatientIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,418
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/962,481
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30 162
; REFERENCE/DOCKET NUMBER: 00786/161.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-463-418-2

```

Query Match 5.0%; Score 99.5; DB 2; Length 496;

Best local Similarity 20.2%; Pred. No. 0.6; Mismatches 117; Indels 95; Gaps 12; Matches 68; Conservative 56; MisMatches 117; Length 1377;

QY 32 PVPSSPAPGLTK----RVKKSQIQLQVTKDGRWKPANDLILNAVIQTLNDLTSVHL 86
Db 170 PVPSSSDNPKLTDAEWYKKQOBESNKVKGILLTNSNPJ---GTMKDKEITNL-- 224

QY 87 GVKSSCFTIREVERWYALLY---DPVSKLACQAMRQLHPEATAAQOSKALFSKAEE 142
Db 225 -VRFVTRKNLHVDEIVATVFAAGDFV-----SVAEVNDVDISENV 268

QY 143 QLSKVGSSNQP-----TLEFQDLI--HRHPDALRATAKAOQAHWLMQKV 190
Db 269 DLHIVVSYSLSKDMGFLPGFRVGVYSSFDNTVSCKMSSRGL----VSSOTOMLASM 322

QY 191 LLEDOTVQPLPKGDQVLNFSDAEIIDDSKLKMDDEVLEHELMVAD----- 237

Db 323 LSDPQFDV-----NF-----LMESSRIGRHKVFITGIKADIACLTNSGLEW 368

QY 238 ---IRQKREIROLFQELHKWQVLVISITGMSSP-----DFDNQTLAVL 277

Db 369 MDRHLRLRNFSFEIELWHIIIRVKLNVSPGSSFRCTEPGWFRICFANMDDDTLHVA 428

QY 278 RGRMRYLUMSRETTIGRATKDQDVDLSLEGRAW 313
Db 429 LGRIODPFVKNKNKIVEKASENDQVTONSAKKLNW 464

RESULT 6
US-08-308-818-4
Sequence 4, Application US/08308818
Patent No. 5847077
GENERAL INFORMATION:
APPLICANT: Green, Michael R
TITLE OF INVENTION: A No. 5847077el Fungal Multisubunit Protein
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,818
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 03442/034404
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-07700
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: D. melanogaster
IMMEDIATE SOURCE:

RESULT 6
US-08-308-818-4
Sequence 4, Application US/08308818
Patent No. 5847077
GENERAL INFORMATION:
APPLICANT: Reese, Joseph C
TITLE OF INVENTION: Complex Critical for Expression of Fungal Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,818
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 03442/034404
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-07700
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

CLONE: TAIFI-250
US-08-308-818-4

Query Match 5.0%; Score 99.5; DB 2; Length 1377;
Best Local Similarity 21.5%; Pred. No. 2.6; Mismatches 100; Indels 97; Gaps 15; Matches 68; Conservative 51; MisMatches 100; Length 1377;

QY 5 GGVVERGRCS-----GSEPSSEKKVSKAPSTPVPPSPA----PAPGLTRVKKSK 51
Db 998 GPADPTGCGEFFSVRVENPKQTKEEQESQ-PKRSVGTDAIDLRLFLQARELLRQPK 1056

QY 52 QPLQVTKDGRWKANDLILNAVIQTLNDLTSPLGV-KFS--CRFTREVERWYALLY 108
Db 1057 VPEEBIKKLSRW---EVIDVVRFLSTEAKAGBEGMDKFPSRGNRFSIAEHQERY---- 1107

QY 109 DPVSKLACQAMRQLHPEATAIO---SKALFSKAEEOLLSKG----- 149

Db 1108 ---KEECQFLDQNRLVASSELVSTDEAASSESDLEKGKLNENMLSNNKSTQ 1162

QY 150 -STSOPTLETFQDLI-----HRHPDALRATAKALQAHWLM----- 186

Db 1163 LSREKEELER-OBLIQOLDEBHGPGSGGAKGAKGKDPGQOMLATMNQGIRLIRTP 1221

QY 187 ---KQVLLEDOTVQPLPKGDQVLNFSDAEIIDDSKLKMDDEVLEHELMVADRQQ- 240

Db 1222 RGNDOCKEYTRVE-TVRROPVIDAVI-----KIRTRKDBQFTKQFATLDEOK 1267

QY 241 --KREIROLEQHLK 253
Db 1268 EEMREKEREKIQEQR 1283

RESULT 7
US-08-468-558-2
Sequence 2, Application US/08468558
Patent No. 5877280
GENERAL INFORMATION:
APPLICANT: Wetmur, James G.
TITLE OF INVENTION: Cloning and Expression of Thermostable MutS Genes and Proteins and Uses Therefor
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,558
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MSM94-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 4.9%; Score 98.5; DB 2; Length 355;

US-08-468-558-2

Best local similarity 21.4%; Pred. No. 1.6;
Matches 83; Conservative 60; Mismatches 133; Indels 11; Gaps 18;

QY 24 KVSKAPSPVPPSPAP-APGLTKRKVKVKSKQPKQVTKOL-GRWKPAIDLINAVLQND 80
Db 236 KATQKSFPLIPKPKPVDEGVVKDLKAVKGLETIESIGR---KOLSLFKVW---D 287

QY 81 LSVHVLGKPKSCPFTL-----REVOERWALLYDPVTSKACAMQRLHPEATAA 130
Db 288 RTITGMG-RRLRFLPFRLLPFRSTERRKVQE---AWEELINK-----REVINE 331

QY 131 IOKSALKFSKAE-HQLSKVGSTSQPTLETFQDOLIHRHPDAFYLAARTAKALOAHWQLMQY 189
Db 332 IR-KTLEGMSDLRKNVRSS---NMASPRELJH-----LKNSLRKAELRKTL 376

QY 190 YILEDQTVQPLPKQGDQVINFSDAEFLIDSKLKDMDRVELEHLMV---AURQQKREIR 245
Db 377 SLDSEITKEIE--GSILANLNKVKADLQKLTIVDPPPLAVKEGGSLIKPGVNAVYDLEBREIR 434

QY 246 Q-LEQELHKWQVLVDSTOMS-----PDF---DNOTLAUVRG 279
Db 435 ENAEKLUKEYEKUKKETQISLKIHQYKNGYIIEVTGANVKKVPERFRQTLNAER 494

QY 280 RMVTRYLMSREITTGRTADNOIDVLD-----SLEGPW 313
Db 495 YTTEELORLEEKILSAQTRINELLEYELYRELREEVVKELDKVGNNAATLIGEVDYIQSLAW 554

QY 314 KLSRKQGVTKLUNGDFFIANGRRPPI 340
Db 555 LALEKGWVTPKEVHEGGYELITEEGKHPV 581

RESULT 8

US-08-676-444-2
; Sequence 2, Application US/08676444A
; GENERAL INFORMATION:
; APPLICANT: Wettur, James G.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF THERMOSTABLE
; FILE REFERENCE: MSM95-02
; CURRENT APPLICATION NUMBER: US/08/676,444A
; CURRENT FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Aquifex pyrophilus
; US-08-676-444-2

Query Match 4.9%; Score 98.5; DB 4; Length 855;
Best Local Similarity 21.4%; Pred. No. 1.6;
Matches 83; Conservative 60; Mismatches 133; Indels 11; Gaps 18;

QY 24 KVSKAPSPVPPSPAP-APGLTKRKVKVKSKQPKQVTKOL-GRWKPAIDLINAVLQND 80
Db 236 KATQKSFPLIPKPKPVDEGVVKDLKAVKGLETIESIGR---KOLSLFKVW---D 287

QY 81 LTSVHVLGKPKSCPFTL-----REVOERWALLYDPVTSKACAMQRLHPEATAA 130
Db 288 RTITGMG-RRLRFLPFRLLPFRSTERRKVQE---AWEELINK-----REVINE 331

QY 131 IOKSALKFSKAE-HQLSKVGSTSQPTLETFQDOLIHRHPDAFYLAARTAKALOAHWQLMQY 189
Db 332 IR-KTLEGMSDLRKNVRSS---NMASPRELJH-----LKNSLRKAELRKTL 376

QY 190 YILEDQTVQPLPKQGDQVINFSDAEFLIDSKLKDMDRVELEHLMV---AURQQKREIR 245
Db 377 SLDESEITKEIE--GSILANLNKVKADLQKLTIVDPPPLAVKEGGSLIKPGVNAVYDLEBREIR 434

QY 246 Q-LEQELHKWQVLVDSTOMS-----PDF---DNOTLAUVRG 279
Db 377 SLDESEITKEIE--GSILANLNKVKADLQKLTIVDPPPLAVKEGGSLIKPGVNAVYDLEBREIR 434

QY 246 Q-LEQELHKWQVLVDSTOMS-----PDF---DNOTLAUVRG 279
Db 377 SLDESEITKEIE--GSILANLNKVKADLQKLTIVDPPPLAVKEGGSLIKPGVNAVYDLEBREIR 434

RESULT 9

US-08-887-534A-85
; Sequence 85, Application US/08887534A
; Patent No. 6455323
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,534A
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1048 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-887-534A-85

Query Match 4.9%; Score 97.5; DB 4; Length 1048;
Best Local Similarity 24.6%; Pred. No. 2.7;
Matches 45; Conservative 35; Mismatches 84; Indels 19; Gaps 7;

QY 116 ACOMQRLHPEATAAIAOKSALKFSKAEHQLSKVGSTSQPTLETFQDOLIHR-HPDAFYLAR 174
Db 516 AVEAVQALEP---GVNQSRILALENEVKLGREGATURQOLAITKQLORDNEAQSIRO 572

QY 175 TAKALOAHWQLMQYKYLEDQTVQPLPKQGDQVINFSDAEFLIDSKLKDMDRVELEHLM 234
Db 573 DEQALTOQOAVIASLNI---TQQPL---DDIQPWLDRQ---DEHERQLRLLSQRHLQ 622

QY 235 VARRQQKREIRQFQEL-HKHWQVLVDSTOMS---MSSPFDIDNOTLAUVRGRMVRYLRSR 289
Db 623 GOTAAHNOQQTQQQQBQRQQLITITGYAULTPQDDEESWLAUTROQENQSQQRON 682

QY 290 EIT 292
Db 683 ELT 685

RESULT 10

US-08-620-717A-9
; Sequence 9, Application US/08620717A
; Patent No. 5670365
; GENERAL INFORMATION:
; APPLICANT: Feltelson, Jerald S.
; TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,717A
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/540,104
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA94.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; FAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 167P
; US-08-620-717A-9

Query Match 4.9% Score 97; DB 1; Length 1168;
Best Local Similarity 25.5%; Pred. No: 3,5; Length 1168;
Matches 51; Conservative 26; Mismatches 89; Indels 34; Gaps 7;

Qy 80 DLTSVHLGVKFSCTRLREVQERWVALYPPVISHLACQAMRQLHEATAIQLSK-ALFS 138
; :|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 901 DVGSIHQSDVNVLGIERGIRIAKPNGLA-----KISHLTEIKDRPLTEKEIKVQRKQWK 955
; ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 139 KAEEOQILSKUGSTSPTLETQFDLHLR-----HPDAFLIARTKAL-----QHWW-- 183
; ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 956 KAFNQEQAETTQTLQPTDQNLNAQNEDNGSVPHVTQHLSAVWPPLPKQRHWFME 1015
; ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 184 -----QLMKQYVLLEDQTQPLPKGDQVNFSPKQEDLD-----DSKLKDM-RDEVLE 230
; ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 1016 DREGSHVWLQQFQALDRAQQIBEONLHNGNFAANGLTDWTVTGDAQLTIFDDDPVLE 1075
; ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 231 HELMADRRQKRETROLEQE 250
; ||:|||:|||:|||:|||:|||:|||:|||:
Db 1076 LAHWDASISOTIEIMDFED 1095
; ||:|||:|||:|||:|||:

RESULT 11
US-09-592-054-2
; Sequence 2, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe

RESULT 12
US-08-740-223A-18
; Sequence 18, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996

APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: motor proteins and methods for
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/592,054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Human
; US-09-592-054-2

Query Match 4.9% Score 97; DB 4; Length 1232;
Best Local Similarity 21.6%; Pred. No. 3,8; Length 1232;
Matches 79; Conservative 58; Mismatches 129; Indels 100; Gaps 17;

Qy 3 ARGGVEPGROSSGPSSSEKKVSKAPSPTPVPSPPAPGAPLTKRKVKSKQPLQVTKDLGR 62
; |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 368 AHGGTLPGSIT-VERPSENLIQSLMKNQSL-VEENKLSRGSLSEAAGQTAQMELRI---I 421
; |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Qy 63 W-KPANDLILINAVIQLNTDSLTHLGVKFRSCRFIREVOERWVALYPPVIS---KLAC- 117
; |:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 422 WTEQANEKM---NAKLE-----ELRQHACKLUDQKVE---TLEQELKVENELCN 468
; |||:|||:|||:|||:|||:|||:|||:|||:
Qy 118 --QAMRQLHPEATA-----AIOSKALFSKABEQLLSSKGVTSQPTLETFO---DILH 164
; |||:|||:|||:|||:|||:|||:|||:|||:
Db 469 LQLQITOLSDETTVACMAAIDTAVEQAEQVETSPESTSRSSDAFTQHAIRQAQMSKELVE 528
; |||:|||:|||:|||:|||:|||:|||:|||:
Qy 165 RHPD-AFYLARTRAKALQAHWQLMKOYILEDQTVQP-----LPKGSDQVLFSDAEDL 215
; |||:|||:|||:|||:|||:|||:|||:
Db 529 LNKALALKEARLKWTQNDSOLOPIQOYOQDNIKEPELEVINTLQEKREBBLVLELQTAKKD 588
; |||:|||:|||:|||:|||:|||:
Qy 216 IDDSKLKDMRDEVL-EHLMVADRQK-----REIRQLEQELHKWQVLVD 259
; |||:|||:|||:|||:|||:|||:
Db 589 ANQAKLSEERRKRQIQLEGQIADLKKKNEQSKULLKESTERTVSKANOEIR----- 641
; |||:|||:|||:|||:
Qy 260 SITGMSSPDPDQNTLAVLRGRMVRYLMRSREITIGRATKDQIDVDSLLEGPAWKISKQ 319
; |||:|||:|||:|||:
Db 642 -----MMKNQRVQJLMRQMKED-----AEKFRQWQKQRDK 670
; |||:|||:
Qy 320 GVIKLK 325
; |||:
Db 671 EVIQLK 676

CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 60/022/999
 FILING DATE: 02-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 503 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FEATURE:
 NAME/KEY: TIE ligand-4
 LOCATION: 1..503
 OTHER INFORMATION:
 US-08-740-223A-18

Query Match 4.8%; Score 95.5; DB 4; Length 503;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 77; Conservative 51; Mismatches 155; Indels 71; Gaps 18;

QY 30 STRVPSPAPAGLTKRVKS-KQPLQVTKDGRWKPANDLILNAVIQTND--LTSVHL 86
 Db 52 SEPCCPGPEVRSNTLQRESLANPLHKG---LPTQQVKOLEQALQNNTQWLKKLER 106

QY 87 GVKFSCRTRLRSEVRWVALLYDPVISKLACQAMRQLRPEATAIQSKAKAEQOLIS 146
 Db 107 AKTILRKLEQVQOQMAQNTAPML-SLGTSLLNQ---TTAQIRK---LTDMEAQLIN 158

QY 147 KVGSTSQPTLETF-----QDLIHRHDAYLARTAKALQAHQWLM-KQYVLEDOTV 197
 Db 159 QTSRMDAQMPETFLISTKLNQOLLQRQKLQLOGNSALEKLOALETQ---QBELA 214

QY 198 QPLPKGDOVLNTSDAELDDSKLDRDEVELEHLMADREKREIRBLQRLBQBLHKWQL 257
 Db 215 SILSKKAKLNTLSROSAALTNTIERGLRG-VHNHSLLQD-OOHSRLQ---LVLLRHL 268

QY 258 VDSITGMSSPPDFDNQTLAVLRGRMV---RYLMRS-----REITGRATCNDQIVDUL 306
 Db 269 VDERRANASAPAF-----IMACRQFDCABEFORSAGSASGYTIVOSNATRKPKVICDL 322

QY 307 SLEGPAWKI--SRKGQVTKLKN-----GDFFIANE-----GRRPY 341
 Db 323 QSGGGRWLILQRRENGTVNFQRNMKDYKQGFDPAGBHWLGNENVHQLTRRAY 376

RESULT 14
 US-09-202-491-10
 ; Sequence 1.0, Application US/09202491
 ; Patent No. 6432667
 ; GENERAL INFORMATION:
 ; APPLICANT: Valenzuela et al.
 ; TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
 ; FILE REFERENCE: REG330-K
 ; CURRENT APPLICATION NUMBER: US/09/202,491
 ; CURRENT FILING DATE: 1998-11-16
 ; EARLIER APPLICATION NUMBER: PCT/US97/10728
 ; EARLIER FILING DATE: 1997-06-19
 ; EARLIER APPLICATION NUMBER: 60/022,999
 ; EARLIER FILING DATE: 1996-08-02
 ; EARLIER APPLICATION NUMBER: 60/021,087
 ; EARLIER FILING DATE: 1996-07-02
 ; EARLIER APPLICATION NUMBER: 08/665,926
 ; EARLIER FILING DATE: 1996-06-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-202-491-10

Query Match 4.8%; Score 95.5; DB 4; Length 503;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 77; Conservative 51; Mismatches 155; Indels 71; Gaps 18;

QY 30 STRVPSPAPAGLTKRVKS-KQPLQVTKDGRWKPANDLILNAVIQTND--LTSVHL 86
 Db 52 SEPCCPGPEVRSNTLQRESLANPLHKG---LPTQQVKOLEQALQNNTQWLKKLER 106

QY 87 GVKFSCRTRLRSEVRWVALLYDPVISKLACQAMRQLRPEATAIQSKAKAEQOLIS 146
 Db 107 AKTILRKLEQVQOQMAQNTAPML-SLGTSLLNQ---TTAQIRK---LTDMEAQLIN 158

RESULT 13
 US-09-202-491-4
 ; Sequence 4, Application US/09202491
 ; Patent No. 6432667
 ; GENERAL INFORMATION:
 ; APPLICANT: Valenzuela et al.
 ; TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
 ; FILE REFERENCE: REG330-K
 ; CURRENT APPLICATION NUMBER: US/09/202,491
 ; CURRENT FILING DATE: 1998-11-16
 ; EARLIER APPLICATION NUMBER: PCT/US97/10728
 ; EARLIER FILING DATE: 1997-06-19
 ; EARLIER APPLICATION NUMBER: 60/022,999
 ; EARLIER FILING DATE: 1996-08-02
 ; EARLIER APPLICATION NUMBER: 60/021,087
 ; EARLIER FILING DATE: 1996-07-02
 ; EARLIER APPLICATION NUMBER: 08/665,926
 ; EARLIER FILING DATE: 1996-06-19
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-202-491-10

Query Match 4.8%; Score 95.5; DB 4; Length 503;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 77; Conservative 51; Mismatches 155; Indels 71; Gaps 18;

QY 30 STRVPSPAPAGLTKRVKS-KQPLQVTKDGRWKPANDLILNAVIQTND--LTSVHL 86
 Db 52 SEPCCPGPEVRSNTLQRESLANPLHKG---LPTQQVKOLEQALQNNTQWLKKLER 106

QY 87 GVKFSCRTRLRSEVRWVALLYDPVISKLACQAMRQLRPEATAIQSKAKAEQOLIS 146
 Db 107 AKTILRKLEQVQOQMAQNTAPML-SLGTSLLNQ---TTAQIRK---LTDMEAQLIN 158

RESULT 15
 US-09-709-188-18
 ; Sequence 18, Application US/09709188
 ; Patent No. 6441137
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis et al.
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
 ; FILE REFERENCE: REG 333-Z
 ; CURRENT APPLICATION NUMBER: US/09-709,188
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 08/740,223
 ; PRIOR FILING DATE: 1996-10-25
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-709-188-18

Query Match 4.8%; Score 95.5; DB 4; Length 503;
 Best Local Similarity 21.8%; Pred. No. 1.4; Mismatches 155; Indels 71; Gaps 18;
 Matches 77; Conservative 51; Mismatches 155; Indels 71; Gaps 18;

Qy 30 STPVPPSPAPGLTKRKKSS-KOLOVTKDGRKPKPNDLILINAVLQTND--LTSVHL 86
 Db 52 SEPCCPGPEVSRDSNLQRSLNPLHKG----LPTQVQKQLQALQNTQMKLKR 106
 Qy 87 GVKFSCRFTRLEVQHVALLYDPYVSKLACQAMQQLHPEATAATQSALKFSKABEOLLS 146
 Db 107 AIKTILRSKLEQVOQOMAQNOTAPML-ELGTSLLNQ---TTAQRK--LTDMEAQLLN 158
 Qy 147 KVGSTSQPTLETF-----QDLIRHHPDAFTLAKALQAHQIM--KOYVILEDQTV 197
 Db 159 QTSRMIDAQMPETFLSTNKLENQLLQROKQLOQCONSALERKLRALETKO---OEELA 214
 Qy 198 QPLPKQDQVANFSDAEDLDDSKLKDMDVELEHLMADRQKEIRIOQEELHKWQVL 257
 Db 215 SILSKKAKLNTLSRQAULTNTERGLRG-VRHNSLQLD-QQSLRQL--LVLRLH 268
 Qy 258 VDSITGMSSPDFDNQTLAVLRGRMV---RYLMRS-----RETLGRATKDNDQIVDVL 306
 Db 269 VQERANASAPF-----IMAGEOFQDCAEIQRSGASASGVYTQVSNAIKPRKVFCDL 322
 Qy 307 SLEGAWKI--SRKGQGVVIKLN-----GDFFTANE---GRRPY 341
 Db 323 OSSGERWTLIQRRENGTUNFORNWWDYKQGFQGDPAEHMLGNENVYHOLTRRAY 376

Search completed: March 27, 2003, 05:23:22
 Job time : 40 secs

Om protein - protein search, using sw model
Run on: March 27, 2003, 05:21:49 ; Search time 30 Seconds
Title: US-09-744-125A-2
Perfect score: 1996
Sequence: 1 NSARGGVEPGRGSGSEPPSS.....LINQDILIALTRAEEKITPQ 390
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 237916 seqs, 5873674 residues
Total number of hits satisfying chosen parameters: 237916
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/podata/1/pubpaa/US08_NEW_PUB.pep:
2: /cgn2_6/podata/1/pubpaa/PCT-NEW_PUB.pep:
3: /cgn2_6/podata/1/pubpaa/US06_NEW_PUB.pep:
4: /cgn2_6/podata/1/pubpaa/US06_PUBCOMB.pep:
5: /cgn2_6/podata/1/pubpaa/US07_NEW_PUB.pep:
6: /cgn2_6/podata/1/pubpaa/US07_PUBCOMB.pep:
7: /cgn2_6/podata/1/pubpaa/PCTUS_PUBCOMB.pep:
8: /cgn2_6/podata/1/pubpaa/US18_PUBCOMB.pep:
9: /cgn2_6/podata/1/pubpaa/US09_NEW_PUB.pep:
10: /cgn2_6/podata/1/pubpaa/US09_PUBCOMB.pep:
11: /cgn2_6/podata/1/pubpaa/US10_NEW_PUB.pep:
12: /cgn2_6/podata/1/pubpaa/US10_PUBCOMB.pep:
13: /cgn2_6/podata/1/pubpaa/US60_NEW_PUB.pep:
14: /cgn2_6/podata/1/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	123.5	6.2	108	10 US-09-764-887-176 Sequence 176, App
2	110.5	5.5	530	9 US-09-764-887-176 Sequence 8, Appli
3	110.5	5.5	530	10 US-09-962-055-8 Sequence 8, Appli
4	110.5	5.5	530	12 US-10-023-529-8 Sequence 8, Appli
5	110.5	5.5	530	12 US-10-023-523-8 Sequence 44, Appli
6	110.5	5.5	546	9 US-09-976-740-44 Sequence 44, Appli
7	110.5	5.5	546	12 US-10-023-529-44 Sequence 44, Appli
8	110.5	5.5	546	12 US-10-023-523-44 Sequence 44, Appli
9	107	5.4	557	9 US-09-976-740-5 Sequence 5, Appli
10	107	5.4	557	10 US-09-962-055-5 Sequence 5, Appli
11	107	5.4	557	12 US-10-023-523-5 Sequence 5, Appli
12	107	5.4	557	12 US-10-023-523-5 Sequence 5, Appli
13	106	5.3	519	10 US-09-833-790-435 Sequence 435, App
14	102.5	5.1	751	10 US-09-864-761-38419 Sequence 30419, A
15	100.5	5.0	475	10 US-09-812-11259 Sequence 11259, A
16	99	5.0	327	10 US-09-777-745-4 Sequence 4, Appli
17	97.5	4.9	1048	10 US-09-741-669-409 Sequence 409, App
18	97.5	4.9	1048	10 US-09-812-142-10062 Sequence 10062, A
19	96	4.8	558	10 US-09-777-745-6 Sequence 6, Appli

ALIGNMENTS

SEQ ID NO.	SEQUENCE
20	94.5 4.7 465 9 US-10-103-806-676 Sequence 675, App
21	94.5 4.7 1033 9 US-09-820-843A-75 Sequence 75, Appli
22	93.5 4.6 277 10 US-09-920-300-1467 Sequence 1467, Ap
23	93 4.7 302 9 US-10-043-487-248 Sequence 248, App
24	92.5 4.6 1312 10 US-09-925-302-678 Sequence 120, App
25	92 4.6 712 10 US-09-925-302-678 Sequence 678, App
26	91.5 4.6 526 10 US-09-777-745-2 Sequence 2, Appli
27	91.5 4.6 1274 9 US-10-020-215-2 Sequence 2, Appli
28	90.5 4.5 573 9 US-10-043-487-327 Sequence 327, App
29	90 4.5 1205 9 US-10-173-123-3 Sequence 3, Appli
30	90 4.5 1207 9 US-10-173-123-4 Sequence 4, Appli
31	89.5 4.5 544 9 US-10-174-590-274 Sequence 274, App
32	89.5 4.5 544 9 US-10-176-758-274 Sequence 274, App
33	89.5 4.5 544 9 US-10-175-737-274 Sequence 274, App
34	89.5 4.5 544 9 US-10-177-705-274 Sequence 274, App
35	89.5 4.5 544 9 US-10-175-738-274 Sequence 274, App
36	89.5 4.5 544 9 US-10-175-752-274 Sequence 274, App
37	89.5 4.5 544 9 US-10-176-482-274 Sequence 274, App
38	89.5 4.5 544 9 US-10-176-917-274 Sequence 274, App
39	89.5 4.5 544 9 US-10-176-913-274 Sequence 274, App
40	89.5 4.5 544 9 US-10-180-552-274 Sequence 274, App
41	89.5 4.5 544 9 US-10-180-557-274 Sequence 274, App
42	89.5 4.5 544 9 US-10-173-700-274 Sequence 274, App
43	89.5 4.5 544 9 US-10-174-572-274 Sequence 274, App
44	89.5 4.5 544 9 US-10-174-579-274 Sequence 274, App
45	89.5 4.5 544 9 US-10-174-582-274 Sequence 274, App

RESULT 1
US-09-764-887-176
; Sequence 176, Application US/09764887
; Patent No. US2002002096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-03-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176 ,
; LENGTH: 108 ,
; TYPE: PRT
; FEATURE:
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (105)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-887-176
; Query Match Score 123.5; DB 10; Length 108;
; Best Local Similarity 71.1%; Pred. No. 0.0015; Mismatches 3; Indels 3; Gaps 2;
; Matches 27; Conservative 3; Mismatches 3; Indels 3; Gaps 2;
; RESULT 2
; US-09-976-740-8
; Sequence 30419, A
; Sequence 11259, A
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE NUMBER: 10797-00401
 ; CURRENT APPLICATION NUMBER: US/09/976,740
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 09/616,289
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FASTSEQ FOR Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 530
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-976-740-8

Query Match 5,5%; Score 110,5; DB 9; Length 530;
 Best Local Similarity 18,3%; Pred. No. 0,2; Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16;
 Qy 1 NSARGGVVERGRCSGSEPSSEKKVSKAPSTPVPPSPA-----PAPG--LTKRVRKKS-- 50
 Db 75 NQGGPGEDGAQGEPAPEDAEKSRTYVARNGEPEPTPVVYGEKEPSKGDPNTTERIROSDE 134
 Qy 51 -----KQPLQVTQKLGRWRPANDLLINAVLT-NDLTSVHLGKFSERFTREVQWRW 103
 Db 135 VGDRIHRRPQEKKAKGLGK-----ITLIMQINTLSTPKEEKLAALCKKYAELLEHR 188
 Qy 104 YALLYDPVSKLACAMQRLHEATAIOSKALFSSKA----- 140
 Db 189 NSQKQMKLQKQSQQLVQE--KDHRGENSKAVLRSKLSCRELQRHNRSLKEEGYOR 246
 Qy 141 --EBQLSKVGSTSQOPTLTFTQDLIHRHDAYFLARTAKALQAHQ-----LMQOY 190
 Db 247 AREEEBKRKEVTSHQVTENDIOLQMEOHNE----RNSKLRQENMELAERLKKLIEQYE 301
 Db 191 LLEDQTQVQPLPKGQDVLNFSDAEDLDDSKLKMDMDEVLEVLHETMADRSQKRETRQLEQE 250
 Qy 302 LREHH-----DKVFKHDLQOQLVDAKLQOQEMLKE----AEERHORE----- 342
 Qy 251 LHKWQVLVSDITGMSSPDFDNQTLAVLGRGMVRMLRSREI--TIGRATKNDQIDVDSL 308
 Db 343 --KDFLKEAVESQRMCELMKKQOETHLKGQQLAUTEKEEFONTLKS---EVFTTF 395
 Db 309 EGPAWKISRQGVKVLKNGDFFTANEGRPRPIYDGRPVLGSKWRLSNNSVVEIASRF 368
 Qy 396 KQEMERMTK--IKKLEKETMY-----RSRMESSENKALLEMAEKT 435
 Qy 369 V 369
 Db 436 V 436

RESULT 3
 US-09-962-055-8
 ; Sequence 8, Application US/09962055
 ; Patent No. US2002005203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; Law, Simon W.
 ; Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/962,055
 FILING DATE: 24-Sep-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/979,608
 FILING DATE: 26-NOV-1997
 APPLICATION NUMBER: US 60/031,930
 FILING DATE: 27-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis
 REGISTRATION NUMBER: 35,965
 REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5981B)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 530 amino acids
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-962-055-8

Query Match 5,5%; Score 110,5; DB 10; Length 530;
 Best Local Similarity 18,3%; Pred. No. 0,2; Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16;
 Qy 1 NSARGGVVERGRCSGSEPSSEKKVSKAPSTPVPPSPA-----PAPG--LTKRVRKKS-- 50
 Db 75 NQGGPGEDGAQGEPAPEDAEKSRTYVARNGEPEPTPVVYGEKEPSKGDPNTTERIROSDE 134
 Qy 51 -----KQPLQVTQKLGRWRPANDLLINAVLT-NDLTSVHLGKFSERFTREVQWRW 103
 Db 135 VGDRIHRRPQEKKAKGLGK-----ITLIMQINTLSTPKEEKLAALCKKYAELLEHR 188
 Qy 104 YALLYDPVSKLACAMQRLHEATAIOSKALFSSKA----- 140
 Db 189 NSQKQMKLQKQSQQLVQE--KDHRGENSKAVLRSKLSCRELQRHNRSLKEEGYOR 246
 Qy 141 --EBQLSKVGSTSQOPTLTFTQDLIHRHDAYFLARTAKALQAHQ-----LMQOY 190
 Db 247 AREEEBKRKEVTSHQVTENDIOLQMEOHNE----RNSKLRQENMELAERLKKLIEQYE 301
 Db 191 LLEDQTQVQPLPKGQDVLNFSDAEDLDDSKLKMDMDEVLEVLHETMADRSQKRETRQLEQE 250
 Qy 302 LREHH-----DKVFKHDLQOQLVDAKLQOQEMLKE----AEERHORE----- 342
 Qy 251 LHKWQVLVSDITGMSSPDFDNQTLAVLGRGMVRMLRSREI--TIGRATKNDQIDVDSL 308
 Db 343 --KDFLKEAVESQRMCELMKKQOETHLKGQQLAUTEKEEFONTLKS---EVFTTF 395
 Db 309 EGPAWKISRQGVKVLKNGDFFTANEGRPRPIYDGRPVLGSKWRLSNNSVVEIASRF 368
 Qy 396 KQEMERMTK--IKKLEKETMY-----RSRMESSENKALLEMAEKT 435
 Qy 369 V 369
 Db 436 V 436

APPLICANT: Lees, Ann M.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001
 CURRENT APPLICATION NUMBER: US/09/976, 740
 CURRENT FILING DATE: 2001-10-12
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: US/09/616, 289
 PRIOR APPLICATION NUMBER: US/09/616, 289
 PRIOR APPLICATION NUMBER: US/08/979, 608
 PRIOR FILING DATE: 1997-11-26
 PRIOR FILING DATE: 1997-11-27
 PRIOR FILING DATE: 1996-11-27
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SEQ ID NO: 44
 LENGTH: 546
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-976-740-44
 Query Match 5.5%; Score 110.5; DB 9; Length 546;
 Best Local Similarity 18.3%; Pred. No. 0.21; Mismatches 150; Indels 111; Gaps 16;
 Matches 77; Conservative 83; MisMatches 150; Index 111; Gaps 16;
 Qy 1 NSARGGVERGRCSSEPSSESSEKKVSKAPSTPPSPS-----PAPG-LITKRVKGS-- 50
 Db 91 NQGGPGEAQGSPAEPAEAKSRTTYVARNGEPEPTPVNGEKEPSKODPNTRBHQDDE 150
 Qy 51 -----KOPLOVTKDLGRWKPKANDLILNAVLIQT-NDLTSVHLGVKUSCRFTIREVOBRW 103
 Db 151 VGDRRHRPQEKKAKGLGKE-----ITLIMOTINTLSTPEEKLAALKYABLLBHR 204
 Qy 104 YALLDPVISKLACQAMQLHPEAIAIQSKALFSKA----- 140
 Db 205 NSQOKMKLQKQKOSOLWB--KOHLRGEHSKAVLARSKLESLCRELQRHNRSLIKEGVOR 262
 Qy 141 --BQLLSKVGSTSQPTLETQFDLILHRHPDAYLARTAKALQAHQO-----LMQYY 190
 Db 263 ARBEEKRKEVITSHFFQVTLNDIOLQMEHNE----RNSKLRQENMELAERLKLUQYE 317
 Qy 191 LLEDQTVPLPKGQDQVNFSDAEDLIDSKLKLMDRDEVIEHELMVARRQKEBIROBEE 250
 Db 318 LREHHI-----DKVKFKHDLOOLQVDAKLUQQAQEMIKE-----AERHORE----- 358
 Qy 191 LLDQTVPLPKGQDQVNFSDAEDLIDSKLKLMDRDEVIEHELMVADRKQKREJRLQEB 250
 Db 318 LREHHI-----DKVKFKHDLOOLQVDAKLUQQAQEMIKE-----AERHORE----- 358
 Qy 251 LHKWQVILVDISITGMSSDFPDNOTLAVLURGRMVRYLMSRREI-TLGRATKDNOIDVDSL 308
 Db 359 --KDFLFLKEAVESORMCCELMKQOBTHLKLQKQALYTFKEFQONTLSKS----EVFTF 411
 Qy 309 EGPWKISRQGVKIKLKNNGDFITANEGRRPIVIDGRPVLCGSKWRLNSNSVLEASURF 368
 Db 412 KOEMEKTICK-KIKLKEETMY-----RSRWESSNKALLEMAEK 451
 Qy 369 V 369
 Db 452 V 452
 RESULT 8
 US-10-023-529-44
 Sequence 44, Application US/10023523
 Patent No. US20020152485A1
 GENERAL INFORMATION:
 Sequence 44, Application US/10023523
 Patent No. US20020152485A1
 GENERAL INFORMATION:
 Sequence 44, Application US/10023523
 Patent No. US20020152485A1
 GENERAL INFORMATION:
 Sequence 44, Application US/10023523
 Patent No. US20020152485A1
 APPLICANT: Lees, Ann M.
 APPLICANT: Law, Robert S.
 APPLICANT: Arjona, Anibal A.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING TITLE OF INVENTION: ATHEROSCLEROSIS
 FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/023,523
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: US/09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US/09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US/08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US/60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US/60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 44
 LENGTH: 546
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-023-523-44
 Query Match 5.5%; Score 110.5; DB 12; Length 546;
 Best Local Similarity 18.3%; Pred. No. 0.21; Mismatches 150; Indels 111; Gaps 16;
 Matches 77; Conservative 83; Mismatches 150; Indels 111; Gaps 16;
 QY 1 NSARGGVVERGRCSSEPSSESKEKKVSKAPSTPPVPPSPA-----PAPG-LTKRKKGK- 50
 Db 91 NOCGPGEDEGAQGPAPEDAEKSRTTYVARNGEPPTPVNGEKEPPSKGDNPTEFEGRSDE 150
 QY 51 -----KOPLOVTKDGLGRWKPANDLLTNAVLOT-NDLTSVHLGVKSFRTLREVOBRW 103
 Db 151 VGRDRHRIHQEKKAKAGLCKE-----ITLUMQTNTLSTPEEKUAAACKYVAELLEBEHRNSOKMKLQQ 204
 Qy 104 YALIYDPVYISKLACQAMQQLHPEAIAATQSALKFSKA----- 140
 Db 205 NSOKQMKLQKOKSOLVOB-KOHRLGEHSKAVLARSKLESLCRELQRHNRSLKEGVQR 262
 Qy 141 --BEGLJSKVGSTSOPTLETQDILHHRHPDATYARTAKALQAHQ-----IMKQYVILLEDQTVQPLPKG 190
 Db 263 AREREKEKEVITSHFFQVTLNDIQLOMEQHNE----RNSKLQEMMELAERLKQKLIROQE 317
 Qy 191 LLEDQDTQVQPLKGQVQVLNFSDAEDLIDDSKLUKMRDEVIEHELMVADRRQKBEIRQLEQBE 250
 Db 318 LRREHI-----DKVFKHKDQLQOQLVDAKUQOQAEMJKE----AERHORE----- 358
 Qy 251 LHKWQVLVDSITGMSSPFDNOTLAVLGRGMVRMLMRSREI-TLGRATKDQIDVDSL 308
 Db 359 -KDFPLIKEBAVESQRMCLMKGQOBTHLKOOLALYTFKBFEEFQNTISKSS----EVFTTF 411
 Qy 309 EGPFAWKISRKGQVTKLUNGDFPTIANEGRRPIYIDGRPVLCGSKWRLSNNSVFEASLRP 368
 Db 412 KQMBEKMTK--IKKLEKETMY-----RSRWESENKALLEMBEKT 451
 Qy 369 V 369
 Db 452 V 452
 RESULT 9
 US-09-976-740-5
 Publication No. US20020194633A1
 GENERAL INFORMATION:
 APPLICANT: Lees, Ann M.
 APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Ariona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 Law, Simon W.
 Ariona, Anibal A.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 FILE REFERENCE: 10797-00401
 CURRENT APPLICATION NUMBER: US/09/676,740
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 09/616,289
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 557
 TYPE: PRT
 ORGANISM: Oryctolagus cuniculus
 US-09-976-740-5
 Query Match 5.4%; Score 107; DB 9; Length 557;
 Best Local Similarity 18.9%; Pred. No. 0.44; Mismatches 137; Indels 114; Gaps 17;
 Matches 76; Conservative 76; Mismatches 137; Indels 114; Gaps 17;
 Qy 16 EDSSEKEKKVSKA-----PSTPV---PPSPAPAPOLTKRKVK-----KQPLQVT 57
 Db 105 BEPDAEKSRAVYARNGRPEPGTPVNGEKEPSKAFG-TEERTSDVGDRHRRPQEK 163
 Qy 58 KOLGRWKPEANDLILNIVLT-NDLTSVHLGVKSFRTLREVOERNVYALLDPVSKLA 116
 Db 164 KAKGKLGE-----ITLUMQTNTLSTPEEKUAAACKYVAELLEBEHRNSOKMKLQQ 217
 Qy 117 CQMRQLHPEATAIQSKALESKA----- 150
 Db 218 SDOVQE-KDHRLGEHSKAVLARSKLESLCRELQRHNRSLKEGVQRAREBKRKEVTS 275
 Qy 151 TSQPTLETQDILHHRHPDATYARTAKALQAHQ-----IMKQYVILLEDQTVQPLPKG 203
 Db 276 HFQMTLNDIQLQMEQHNE----RNSKLQEMMELAERLKQKLIROQE 323
 Qy 204 DQYLNFSADAEDLIDDSKLUKMDRDEVIEHELMVADRRQKRETRQLEQBLHKWQVLDLSITG 263
 Db 324 DKVFKHKDQLQOQLVDAKUQOQAEMJKE----AERHORE-----KDFPLKEAVES 369
 Qy 264 MSSPFDQMTLAVLGRGMVRMLMRSREI-TLGRATKDQIDVDSL 321
 Db 370 QRNCMLQKQETPLKQOLALYTFKBFEEFQNTISKSS----EVFTTFQEMRMTK--I 422
 Qy 322 IKKUNGDFPTIANEGRRPIYIDGRPVLCGSKWRLSNNSVETIA 364
 Db 423 KUKEKETMY-----RSRWESENKALLEMA 447
 RESULT 10
 US-09-962-055-5
 Sequence 5, Application US/09962055
 Patent No. US20020052033A1
 GENERAL INFORMATION:
 APPLICANT: Lees, Ann M.
 APPLICANT: Lees, Robert S.
 Ariona, Anibal A.
 Law, Simon W.
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/962,055
 FILING DATE: 24-Sep-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/979,608
 FILING DATE: 26-Nov-1997
 APPLICATION NUMBER: US 60/031,930
 FILING DATE: 27-Nov-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis
 REGISTRATION NUMBER: 35,965
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 557 amino acids
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-962,055-5

Query Match 5.4%; Score 107; DB 10; Length 557;
 Best Local Similarity 18.9%; Pred. No. 0 44; Mismatches 137; Indels 114; Gaps 17;
 Matches 76; Conservative 76; MisMatches 137; Indels 114; Gaps 17;

QY 16 EPSSSEKKVSKA-----PSTPV---PPSPAPAGLTKRVKS-----KQPLQVT 57
 Db 105 EPEDAEKSRAVARNGPBPGLPVNGKEKTSKAEGP---TEERTSDDEVGDHRHRRQEK 163
 Qy 58 KDLGRWKPKANDLILNIAVLQT-NDLTSVHLGVKFSCRTLREVQERWYALLYDPVTSKLA 116
 Db 164 KAKGLGKE-----ITLIMQTLNTLSPEEKLAALCKKYAELLEBHRNSQKOMKLQKQ 217
 Qy 117 COAMRQLRPEATAIQSKALSKA-----EQQLSKVGS 150
 Db 218 SOLVOE--KOHLRGENSKAILARSKLESCLQRINRSLKEBGVORAREBEBKRKEVTS 275
 Qy 151 TSOPTLTFDQLLHRPDAFYLARTAKALLQAHWQ-----LMKQYVILEDOTVQPLPKG 203
 Db 276 HfqMTLNDIQLQMEQNE-----RNSKLQEMMELAERLKQJIEQVBLREHI----- 323
 Qy 204 DQVLNFSDAEDLIDDSKLUKMDRDEVIEHELMVADROKRETRQLEQBHKMQLVLSITG 263
 Db 324 DRVKHKHDQQLQVDAKLQQAEMLE-----AEERHORE-----KOFLLKAVES 369
 Qy 264 MSSPDDFNQNOTLAVLRGRMRVIRMSREI--TIGRATKDQIDVDSLIEGPAWKISKQGV 321
 Db 370 ORMCCELMKQOETHLHQOLALYTERKEFFONTLSS-----EVFTFPQEMEKMTK--I 422
 Qy 322 IKLKNNDFFIANEGRRPIVLDGRPVLCGSKWLNSNVWEA 364
 Db 423 KKLKEKETMY-----RSRWESENKALLEMA 447

RESULT 11
 US-10-023-529-5
 Sequence 5, Application US/10023529
 Patent No. US20020129388A1

GENERAL INFORMATION:
 APPLICANT: Lees, Ann M.
 APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 TITLE OF INVENTION: ANTHROSCLEROSIS
 CURRENT APPLICATION NUMBER: US/10/023,523
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: US/09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 60/048,547
 PRIOR FILING DATE: 1997-06-03
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: FastSEQ for Windows Version 4.0

Query Match 5.4%; Score 107; DB 12; Length 557;
 Best Local Similarity 18.9%; Pred. No. 0 44; Mismatches 137; Indels 114; Gaps 17;
 Matches 76; Conservative 76; MisMatches 137; Indels 114; Gaps 17;

QY 16 EPSSSEKKVSKA-----PSTPV---PPSPAPAGLTKRVKS-----KQPLQVT 57
 Db 105 EPEDAEKSRAVARNGPBPGLPVNGKEKTSKAEGP---TEERTSDDEVGDHRHRRQEK 163
 Qy 58 KDLGRWKPKANDLILNIAVLQT-NDLTSVHLGVKFSCRTLREVQERWYALLYDPVTSKLA 116
 Db 164 KAKGLGKE-----ITLIMQTLNTLSPEEKLAALCKKYAELLEBHRNSQKOMKLQKQ 217
 Qy 117 COAMRQLRPEATAIQSKALSKA-----EQQLSKVGS 150
 Db 218 SOLVOE--KOHLRGENSKAILARSKLESCLQRINRSLKEBGVORAREBEBKRKEVTS 275
 Qy 151 TSOPTLTFDQLLHRPDAFYLARTAKALLQAHWQ-----LMKQYVILEDOTVQPLPKG 203
 Db 276 HfqMTLNDIQLQMEQNE-----RNSKLQEMMELAERLKQJIEQVBLREHI----- 323
 Qy 204 DQVLNFSDAEDLIDDSKLUKMDRDEVIEHELMVADROKRETRQLEQBHKMQLVLSITG 263
 Db 324 DRVKHKHDQQLQVDAKLQQAEMLE-----AEERHORE-----KOFLLKAVES 369
 Qy 264 MSSPDDFNQNOTLAVLRGRMRVIRMSREI--TIGRATKDQIDVDSLIEGPAWKISKQGV 321
 Db 370 ORMCCELMKQOETHLHQOLALYTERKEFFONTLSS-----EVFTFPQEMEKMTK--I 422
 Qy 322 IKLKNNDFFIANEGRRPIVLDGRPVLCGSKWLNSNVWEA 364
 Db 423 KKLKEKETMY-----RSRWESENKALLEMA 447

RESULT 12
 US-10-023-523-5
 Sequence 5, Application US/10023523
 Patent No. US20020152482A1

GENERAL INFORMATION:
 APPLICANT: Lees, Ann M.
 APPLICANT: Lees, Robert S.
 APPLICANT: Law, Simon W.
 APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 TITLE OF INVENTION: ANTHROSCLEROSIS
 CURRENT APPLICATION NUMBER: US/10/023,523
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: US/09/616,289
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: US 09/517,849
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: US 08/979,608
 PRIOR FILING DATE: 1997-11-26
 PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SBQ ID NO: 5
LENGTH: 557
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-10-023-523-5

Query Match 5.4%; Score 107; DB 12; Length 557;
Best Local Similarity 18.9%; Pred. No. 0.44; Mismatches 76; Conservatiive 76; Indels 114; Gaps 17; Matches 76;

Qy 16 EPSSSEKKVSKA-----PSTPV-----PPSPAPGLTAKRVS-----KQPLQVT 57
Db 105 EPEDERAKSRYVARVNGERPERGTPVNGEKEKTSKAPG-TEEIRUTSDEVGDRDHRRPKK 163

Qy 117 COAMRQLRPEATAAIOSKALFSKA-----EBOLISKYGS 150
Db 218 SQLVQE--KDLHRLGEHSKAILRSKLESLCRELQRHNRSLKEEGVQRAREEEERRKEVTS 275

Qy 151 TSGPTLETFOPDLLHRHPDAFLARTAKALQAHQ-----LMKQXYLEDQVQVPLPKG 203
Db 276 HFQONTLNDILOLQOMQHNE-----RNSKURQENNMIAERLUKKLEFOYERBHT----- 323

Qy 204 DQVQNFSDAELDDSKUKMORDEVLEHEMLADRRQKEIROLEQELHKWQVLDVSI TG 263
Db 324 DKVFHKHQDQQQLVDAKLOQAQEMIKE-----AEFHORE-----KDFLKEAVES 369

Qy 264 MSSDPFDNOTLAVERGRGMVYLMERSREI--TLCRATKONOIDVYLISLGSPAWKLSRKGV 321
Db 370 ORMCCELMKOQETHLKKQOLAYTEKEFONTLSKS-----EVFTTFKQEMEKMTRK--I 422

Qy 322 IUKLNGNPFPIANERGRRPIYIDGRPVLCOSKWLNSNVIA 364

Db 423 KKLFRKETTY-----RSRWESENKALLEMA 447

RESULT 13
US-09-833-790-435 Application US/09833790
; GENERAL INFORMATION:
; Sequence No. US20020063288A1
; PATENT NO. US20020063288A1

APPLICANT: Iodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indrias, Carol Y.
APPLICANT: Fan, Lijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SBQ ID NO: 435
LENGTH: 519
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-790-435

Query Match 5.3%; Score 106; DB 10; Length 519;
Best Local Similarity 21.8%; Pred. No. 0.49; Mismatches 87; Conservatiive 57; Indels 112; Gaps 20;

Qy 62 RMKPANDLILINAVL---QTNDLTsv--HLGVKFSCRIPTREVQWALLYDPVISK 114

Db 8 RTMPAVDKULLERALOJSPOTSLSLSFEEADGTLTDYTNQLIQAMORYVGQNE----- 62
Qy 115 LAQAMRQJLHPPEAAIOSKALFSKAEQQLSKRUGSTSQPTLETQDQLLHRPDAFYLAR 174
Db 63 -MCUATQOOLSKOLAYERONFAFLGKGEBEVIS----- 174
Db 101 VVBLNLUHTEAKQ----LADTMVLP-----IIQFRE-KDITEVSTIKDGLGLASNEHD 150

Qy 233 LM-----VADRORREIREIROLEQ-----ELHKGQVLVISIT 262
Db 151 LSMAKYSRLPKKKEKENEKVTEVGKEVAARRKOHLSLOYCAGNALQYKOMAMPEMI 210

Qy 263 GMS--SPFDNQTLAVLRGRMMYR-----MRSEETIG-----RATKDQIDVDSL 308
Db 211 GFAGQGINFFKKGAEFMFKPSFLSSVADMSQIOVEALEAKRMVSQBILSVBSV 270

Qy 309 EGP-----AWKLSR-----KQGVTKLKNQGDFFTANEGRPRIVTDGRPVLC-----GS 351
Db 271 YTFDSVDAAPQINRNLOKAGVNLNLRKWTGLTTWBRLYFTQGGNLMCQPRGAVAGGL 330

Qy 352 KWILSNNSV--VETASLRFVELI--NODLILRAERAK 386
Db 331 IQQLDNCVMSVADCEDRRYCFQITTPNQKGIIQABSRK 370

RESULT 14
US-09-864-761-38419 Application US/09864761
Sequence 39419, Application US/09864761
PATENT NO. US20020049763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wansheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Asonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,455
PRIOR FILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00657
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00654
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00659
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00655
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00651
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00652
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00651
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608, 408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774, 203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SEQ ID NO: 38419
 LENGTH: 751
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL049872.3
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.72
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN EST HUMAN HIT, ALU38211.1, EVALUE 2.00E-83
 OTHER INFORMATION: SWISSPROT HIT: O10411, EVALUE 3.00E-18
 ; US-09-864-761-38419

Query Match 5.1%; Score 102.5; DB 10; Length 751;

Best Local Similarity 20.4%; Pred. No. 1.7; Mismatches 84; Conservative 70; MisMatches 128; Indels 129; Gaps 19; Matches 237

QY 1B SSSEKKVKSKAPSTPVPPSAPAPCILTR-----VKKSKPQPLQVTKRVKKSQKPLQVTKDGLG-----65
 Db NGSEBHDLSKATERL-----VKQKJKELEKILUNENKNISLTQIDOLSKDKEVGK-- 287

QY 66 ANDILLINALQNDLITVHGVKSCRFIREV----QERMVALLPVISKACQM 120
 Db 288 -----LTOIQQDKEIQALHARISSTSHTQDVYLQQLQAMERERKVAVLNKEUR 341

QY 121 RQLRHEA-----IAAISKALFSSKAE--OLISKVGSTSQOPTI-ETFDOL--LHRHPD 168
 Db 342 ENSHKTEVKKMIVAAKEAALIKQDENWKLSTRPESQGDMDRETQNLSPKIREQD 401

QY 169 AFY--LARTAKALOHWOLMKOYILEDOTVOPLKGDGY--LAFSDAIDLDD-SKLUK 223
 Db 402 IEIDLALKQCTLLA-----VIQTSSTGTNEAGGVANSNQFBLLOERDKLHQ 447

QY 224 M-RDEVEHLHMVADRKREBEIRLEQELHKW-QVJDSITGMSSPEDNQDILAVLRG 279
 Db 448 QVKKNEEWKQKQVMVTYNNMHOESAQLOEELHOLQDQVLVD-----DNNSKL--- 494

QY 280 RMVRVLMRSREITIGRATKONQIDVDSLQEGPAWKSRSKQGVKLNNGDPFIANEGRPP 339
 Db 495 -----QVDTGQI-----SYEMETKKN----- 514

QY 340 IYIDCRPVLGSKWNLNSNWSVETASLRFVFLINDQDIALTRABAKITPO 390
 Db 515 -----FGQELAQVOHSGQLQNTKDQDILGKUDISPOLSSASLITPO. 556

RESULT 15
 US-09-815-242-11259
 Sequence 11259, Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Hasebeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yammoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 FILE REFERENCE: BLTRA.01A
 CURRENT APPLICATION NUMBER: US/09/815, 242
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206, 848
 PRIOR FILING DATE: 2000-05-3
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 11259
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 ; US-09-815-242-11259

Query Match 5.0%; Score 100.5; DB 10; Length 475;

Best Local Similarity 19.1%; Pred. No. 1.3; Mismatches 62; MisMatches 136; Indels 157; Gaps 18; Matches 84; Conservative 62; MisMatches 157; Gaps 19;

QY 14 GSEPSSEKKVKSKAPSTPVPPSAPAPCILTR-----AYVNDCGAFSRMQRGQCSA 44
 Db 7 GKLSITANTENMKAPKT----- 44

QY 62 -RKPKANDLILNAVLQNDLITSVHGVKSCRFIREVQEWYALLYDPVISKACQA 119
 Db 45 CKAWNTITEVRLISTAKSKRNDRFSGYAGSTQKIQTSBI----- 84

QY 120 MROLHPPEATAIAISKALFSSKAEOLLSKVGSTSQOPTFQDQLRHDAYFLARTKAL 179
 Db 85 -----SLOTPRSSGFSFSLDRVGGGIVPGSAI--LIGGHGA--GKSTULL 128

QY 180 QAHWMLKO--YVLEPDOTVOPLKGDQVNLNSDAEULIDDSKLDKMRDEVLEHLMVA 236
 Db 129 QVMCGLAKMTALVTVGEBSLQVAMRASLG-----LPSDOLKMLSETSYEQICLA 181

QY 237 DRDKREBROLEQELHKMVLVISITGMSSPFDNOTLAVLRG---MVRVIMRREI 291
 Db 182 D-----QKPKOI---IVDSDIQVHMLADIOSPGSVAOVRECASFILTY-AKTRQV 228

QY 292 TL---GRATKD-----NOIDVDSLQEGPA---WKISR----- 317
 Db 229 AITMGHVTKDGTLAGPKYLEHAJDCSILLEGDRASRTRSHKRFGAVNLGVGMT 288

QY 318 KOVTKLKONGFFIANEGRPRIVIDGREVLCCSK---WRISNNSNVIEIASL----- 366
 Db 289 EGQLEREVKOPSAIFSLR-----GOBITSGSVWMLWEGRPLVIEQALVQDHMSLA 339

QY 367 --REVFLQNDQDIALIRA 382
 Db 340 NPPRVAVGLEQNRLALLIA 358

Search completed: March 27, 2003, 05:29:56
 Job time : 34 secs

RESULT 2
T47594 hypothetical protein T12E18.40 - *Arabidopsis thaliana* (mouse-ear cress)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47594
R;Bloesser, H.; Meves, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.Mewes,
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224469
A;Accession: T47594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-735 <BL0>
A;Experimental source: cultivar Columbia; BAC clone T12E18
C;Genetics:
A;Map position: 3
A;MDP: 27/2; 56/3; 570/3; 588/1; 637/3; 666/3; 709/3
A;Note: T12E18.40

Query Match 10.3%; Score 205; DB 2; Length 735;
Best Local Similarity 32.6%; Pred. No. 1.3e-06; Mismatches 63; Indels 18; Gaps 4;
Matches 56; Conservative 35; Mismatches 63; Indels 18; Gaps 4;

Qy 208 NFSDAEIDLDDSKK-DMRD---EVLEHELMVADRRQKRREIRQLQELHKWQVLVDST 262
Db 563 NYSDTEAMLMDLDPDDQDNFDLKVSKYQ---SQDMKRTIIRLEQAANSYMQRAIAS 618

Qy 263 GMSSSDPDRNGLAVLRGRMVRYLMSREITLGRATKDNDQDVLSLEGPAWKISKQGV 322
Db 619 G-----AFAVLYGGRYKRYKPKPEVLVGRS- 669

Qy 323 KLNKNQDPFFIANEGRPRPIYIDGRPVLCGSKWRLSNSVVEASLRFVFLNQ 374
Db 670 RLGGDGFSFHTKNLGYKSYISIENEKEVDPGQSLIKSDCLVNEIRGMFIEEQNQ 721

RESULT 3
D96622 hypothetical protein F8A5.22 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: D96622
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R;Theology, A.; Ecker, J.R.; Palm, C.J.; Peeterspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Greasy, T.H.; Dewar, K.; anser, N.F.; Hughes, B.J.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Cai, J.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Sun, H.; Tallon, A.; ker, M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-551 <ST0>
A;Cross-references: GB:AL005173; NID:92462740; PIDN:AAH71959.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8A5.22
A;Map position: 1

Query Match 7.1%; Score 142; DB 2; Length 551;
Best Local Similarity 23.5%; Pred. No. 0.025; Mismatches 73; Indels 42; Gaps 4;
Matches 47; Conservative 38; Mismatches 73; Indels 42; Gaps 4;

Qy 211 DAEDLID-DSKLK----DNRDEVLEHELMVADRRQKRREIRQLQELHKWQVLVDST 263
Db 339 DGEEDIDIDAMIRKLNLVPDDSDSCFNREEWMSKHPHALIGQ-----CTRTS 389

Qy 264 MSSPPFDNQTLAVLRRGRMVRYLMSREITLGRATKDNDQDVLSLEGPAWKISKQGV 323

RESULT 4
T39607 fork head protein type transcription factor - fission yeast (*Schizosaccharomyces pombe*)
A;Cross-references: EMBL:AL023554; PIDN:CAA19034.1; GSPDB:GN00067; SPDB:SPBC16G5.15C
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39607
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21866
A;Accession: T39607
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-642 <LYN>
A;Cross-references: EMBL:AL023554; PIDN:CAA19034.1; GSPDB:GN00067; SPDB:SPBC16G5.15C
A;Experimental source: strain 972b-; cosmid c16G5
C;Genetics:
A;Gene: SPDB:SPBC16G5.15C
A;Map position: 2
A;Introns: 17/12

Query Match 5.8%; Score 116.5; DB 2; Length 642;
Best Local Similarity 24.0%; Pred. No. 1.9; Mismatches 43; Conservative 42; Mismatches 77; Indels 17; Gaps 6;

Qy 210 SDAEIDLDDSKKLMRD---EVLEHELMVADRRQKRREIRQLQELHKWQVLVDST 264
Db 8 SKSEHISDDBERKQBDLYKKMDVDTDRNIVLNGRLSIAKLSVUPPHMRVWDDYSNK 67

Qy 265 SSPDFDN---OTLAVLRRGRMVRYLMSREITLGRAT----KDNQIDV-DLSLEGPAWK 314
Db 68 NAERHSGELOAVAKFAGSTWTVYVKKIRILGRPANTPSPKGKQDLEVIDMMF-GPSKV 126

Qy 315 ISRKQGVKIK-NNGDDFFIANEGRPRPIYIDGRPVLCGSKWRLSNSVVEASLRFVLI 372
Db 127 VSKRHAHVVEYDDOTWNCSVYGRNGKIKVDGKLFKNGETVKLTSGSILEVAGLMMFV 185

RESULT 5
AE2417 hypothetical protein alr4893 [imported] - *Nostoc* sp. (strain PCC 7120)
C;Species: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
A;Note: *Nostoc* sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2417
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, T.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen Fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
A;Reference number: AB1807; MUID:2159285; PMID:11759840
A;Accession: AE2417
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-676 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76592.1; PID:917134030; GSPDB:GN00179
C;Genetic:
A;Gene: alr4893

Query Match 5.8%; Score 116; DB 2; Length 676;
Best Local Similarity 19.8%; Pred. No. 2.2; Mismatches 69; Conservative 64; Mismatches 126; Indels 90; Gaps 14;

A;Authors:	Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	Qy	277 TNQSPYDEKLWVFCGSMRHSISQVLSLDDLAAYVDAASDODOKLSSLAGPVLVATIKEH 336
A;Authors:	Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
A;Title:	Sequence and analysis of chromosome 1 of the plant Arabidopsis.	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
A;Reference number:	A86141; MUID:21016719; PMID:1130712	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
A;Accession:	A96494	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
A;Status:	preliminary	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
A;Cross-references:	GB:AE005173; NID:96691192; PIDN:AAF24530.1; GSPDB:GN00141	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
A;Molecule type:	DNA	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
A;Map position:	1	Qy	319 QGVIKLKGNGDFFIAMBGRRPYIDSRPVLGCGSKWRLS--NNSVVETASLRPVFLINQDL 376
Query Match	5.6%; Score 111; DB 2; Length 804;	Db	488 EKLASQNGGERFSWNKLNR-----LC---WAVGSISGTMVPEDEKEKFRLVYRDL 534
Best Local Similarity	23.0%; Pred. No. 6.4;	Qy	377 IAIIRAAK 386
Matches	67; Conservative 41; Mismatches 60; Indels 11; Gaps 11;	Db	535 LGCEQKRKG 544
Qy	97 REVQERMYAL--LYDPVISKLAQCAQMROHQH-PEATAIAIOSKALFSKRAEQLISKNGSTS 152	Db	421 TGMSSPPDNOTIAVL-RGMVRYMRSRE-ITLGATRKONQIDVLSLEGPAWISRK 318
Db	47 RAMTERVELDVEDVEYMEPQTTRATKLHKBDILPTEEYVRLFKLFNEFCSTRYPCSTS 106	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
Qy	153 OPTLETQDPLLHRHPDAFYLARTAKALQAHWQMLKQVYLLQTVQVLPKGQVQVNLNSDA 212	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
Db	107 LAQQLGLLEDVQH----LYQSCHLDTMAY----PVYAWEDETIQPLSTLQVQLYQGM 156	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
Qy	213 EDLUDSKKDMRDEVLEHELMWADRR-----QREBIRQEOLHKWQ 255	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
Db	157 SPDELDCGIGFLFRPSVHCHYRULSIKUGLRFQPSGTGGSKKQYVEREFLKD-----WI 210	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
Qy	256 VLVDSTGTMSSPDFNDNTAFLAVLRGRMVRYLMR-----SREITLGRATKDNOIDVDSL 308	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
Db	211 TIGSSVPVLNASRSKSNO---IRSPVIRYFORSVANVLYSREIT-GTWTNSMEMIAMAL 265	Qy	319 QGVIKLKGNGDFFIAMBGRRPYIDSRPVLGCGSKWRLS--NNSVVETASLRPVFLINQDL 376
Qy	309 EGPAWKISRKGQVYKILKINGDFPIANEGRRPIVIDGPVLCGSK-WRLSN 358	Db	488 EKLASQNGGERFSWNKLNR-----LC---WAVGSISGTMVPEDEKEKFRLVYRDL 534
Db	266 -----KOTLRTQKNGMSLQGKVNTPLSILLIHLCCYKSWAVSN 306	Qy	377 IAIIRAAK 386
RESULT 9		Db	535 LGCEQKRKG 544
G89113	protein ZK42.1 (imported) - Caenorhabditis elegans	Db	421 TGMSSPPDNOTIAVL-RGMVRYMRSRE-ITLGATRKONQIDVLSLEGPAWISRK 318
C;Species:	Caenorhabditis elegans	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
C;Date:	10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
C;Accession:	G89113	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
C;Title:	The C. elegans sequencing Consortium.	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
Science 282, 2012-2018, 1998		Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
A;Title:	Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
A;Reference number:	A75000; MURP_009613; PMID:8531916	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
A;Note:	see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
A;Note:	published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
A;Accession:	G89113	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
A;Status:	preliminary	Qy	319 QGVIKLKGNGDFFIAMBGRRPYIDSRPVLGCGSKWRLS--NNSVVETASLRPVFLINQDL 376
A;Molecule type:	DNA	Db	488 EKLASQNGGERFSWNKLNR-----LC---WAVGSISGTMVPEDEKEKFRLVYRDL 534
A;Residue:	1-1140 <STO>	Qy	377 IAIIRAAK 386
A;Cross-references:	GB:chr_V; PIDN:AAB04981.1; PID:91465818; GSPDB:GN00023; CESP:ZK742.1	Db	535 LGCEQKRKG 544
C;Genetics:		Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
C;Gene:	ZK742.1	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
A;Map position:	5	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
C;Superfamily:	Arabidopsis thaliana exportin 1	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
Query Match	5.3%; Score 106.5; DB 2; Length 4574;	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
Best Local Similarity	23.5%; Pred. No. 1.5e+02;	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
Matches	70; Conservative 52; Mismatches 119; Indels 57; Gaps 13;	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
Qy	122 QLHPEA-TAAQSKAESKAEQULSKVGSNSQPTBTQFQDILHRRPDAFYLTAKALQ 180	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
Db	2488 KLOQBEAKUQLQKSBEMOTVQOBQDQETQALQOQSFSEKSDLQLR--ERFEQEKAQLE 2545	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
Qy	181 AHW-QLMKQVYLLDQDVTQPLPKGDQVNLNSDAEDJDDSKKDMRDEVLEHELMWADRR 239	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
Db	2546 LFODEEVAQAOQLREEQORQ-----QOMEQERQRQLV--ASMEEARR--QHEAEVGR 2595	Qy	163 LHRHPDAPYLARTAKAL---QAH---WLMKQVYLLDQTOVPLPKGDQVNLNSDAED-- 214
Qy	240 QRERIRQEOLHKWQVLYDSTGTMSSPDFNDQ---TAVLURGRMVRYLRSREITLGR 295	Db	337 VALIEVTEPLTEAKLIMRSHDYAQOLLKLTILREMEV-----FVKCLDCWC 385
Db	2596 KQREBLQEQDQRQEQBIL-----ENQRLBOLQLEBORAALAHSEEV-TASQ 2646	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
Qy	296 --ATKDNQIDVLDLSLEGPAW-----ISRKQVYKILKINGDFPIANEGRRP----- 340	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431
Db	2647 VAATKTPLENGRD-ALDGPAAEAEPERSFDGURKVSQRLQZBAG--ILSAEELQRLQHT 2704	Qy	319 QGVIKLKGNGDFFIAMBGRRPYIDSRPVLGCGSKWRLS--NNSVVETASLRPVFLINQDL 376
RESULT 11		Db	488 EKLASQNGGERFSWNKLNR-----LC---WAVGSISGTMVPEDEKEKFRLVYRDL 534
A59404	protein [imported] - human	Qy	377 IAIIRAAK 386
C;Species:	Homo sapiens (man)	Db	535 LGCEQKRKG 544
C;Date:	01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002	Qy	215 -----LIDDSKUKDMRDEVLEHELMWADRO---KREBIRQEOLHKWQVLYDSTI 261
C;Accession:	C59404; A59404	Db	386 WILTAEYLICPFIQPSLYGMMQSQRVH---PRQLYREYLSQRSTM-----I 431

A;Title: Exon structure of the human dystrophin gene.
A;Reference number: 154186; MUID:93300536; PMID:3114593
A;Accession: 154186
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 994-1411 <REF>
A;Cross-references: GB:105642; NID:9181892; PIDN:AAA74506.1; PID:9950344
A;Accession: 168509
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 1776-1913 <REF>
A;Cross-references: GB:105646; NID:9181896; PIDN:AAA74507.1; PID:9950345
A;Accession: 168510
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 2550-2979 <REF>
A;Cross-references: GB:105649; NID:9181899; PIDN:AAA74508.1; PID:9950346
A;Title: Determination of the exon structure of the distal portion of the dystrophin gene.
A;Reference number: 154175; MUID:92372062; PMID:1505985
A;Accession: 154175
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Molecule type: DNA
A;Residues: 2860-3685 <REF>
A;Cross-references: GB:166903; NID:9181881; PIDN:AAA35779.1; PID:9457519
R;Brenepur, J.; Hillers, M.; Junkes, B.; Pfordt, M.; Schlinger, E.; Vosberg, H.P.
Genomics 10, 551-557, 1991
A;Title: Analysis of a dystrophin gene deletion by amplification of mRNA isolated from D
A;Reference number: 154166; MUID:9136530; PMID:1889805
A;Accession: 154166
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2250-2254 <REF>
A;Cross-references: GB:SS4699; NID:9235303; PIDN:AAH19754.1; PID:9235304
R;Feneer, C.A.; Koenig, M.; Kunkel, L.M.
Nature 338, 505-511, 1989
A;Title: Alternative splicing of human dystrophin mRNA generates isoforms at the carboxy A;Reference number: S03902; MUID:89181947; PMID:2648158
A;Accession: S03902
A;Molecule type: mRNA
A;Residues: 'MDP', 12-32-3377-3408 <REF>
C;Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the plasma membrane.
C;Comment: Defects in dystrophin are responsible for the Duchenne/Becker muscular dystrophy.
C;Genetics:
A;Gene: GDB:DMO
A;Cross-references: GDB:119850; OMIM:310200
A;Map position: Xp21.2-p21.2
A;Introns: 11/1; 31/3; 62/3; 88/3; 119/3; 177/2; 217/1; 277/3; 320/3; 383/3; 444/2; 494/3; 305/1; 3075/2; 3096/1; 3121/1; 3217/1; 3265/3; 3325/2; 3362/3; 3408/2; 3421/3; Note: the list of introns is incomplete
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin C;Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; leucine-rich elix
F;1-4-233/Region: hinge
F;53-327/Region: hinge
F;338-447/Region: spectrin/dystrophin repeat homology <SP01>
F;448-556/Region: spectrin/dystrophin repeat homology <SP02>
F;58-667/Region: spectrin/dystrophin repeat homology <SP03>
F;688-717/Region: hinge
F;718-828/Region: spectrin/dystrophin repeat homology <SP04>
F;836-934/Region: spectrin/dystrophin repeat homology <SP05>
F;938-1055/Region: spectrin/dystrophin repeat homology <SP06>
F;047-1154/Region: spectrin/dystrophin repeat homology <SP07>
F;1155-1263/Region: spectrin/dystrophin repeat homology <SP08>
F;265-1367/Region: spectrin/dystrophin repeat homology <SP09>
F;1372-1477/Region: spectrin/dystrophin repeat homology <SP10>
F;1478-1568/Region: spectrin/dystrophin repeat homology #status atypical <SP11>
F;1570-1676/Region: spectrin/dystrophin repeat homology <SP12>
F;1678-1782/Region: spectrin/dystrophin repeat homology <SP13> #status atypical <SP14>
F;1876-1982/Region: spectrin/dystrophin repeat homology <SP15>

RESULT 13
T28667
dynein beta heavy chain - Paramaecium tetraurelia
C;Species: Paramaecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Mar-2001
C;Accession: T28667; PC4340
R;Kandl, K.A.; Forney, J.D.; Asai, D.J.
submitted to the EMBL data library, January 1995
A;Description: The dynein genes of Paramaecium: the differential expression of axonemal a
A;Reference number: Z20502
A;Accession: T28667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4588 <KAN>
A;Cross-references: EMBL:U19464; NID:9625089; PID:9625090; PIDN:AAA61680.1
R;Asai, D.J.; Beckwith, S.M.; Kandl, K.A.; Keating, H.H.; Tjandira, H.; Forney, J.D.
J. Cell Sci. 107, 839-847, 1994
A;Introns: 43/2, 113/3; 171/3; 4490/1
C;Superfamily: dynein heavy chain, cilialy
C;Keywords: nucleotide binding; P-loop
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Query Match 5.2%; Score 104.5; DB 2; Length 458;
 Best Local Similarity 21.1%; Pred. No. 2,le+02;
 Matches 59; Conservative 58; Mismatches 72; Indels 91; Gaps 17;

Qy 48 KKSQKPLQYTKDGLGRWKPANDL-LINAVQTLNTLSVHLGVKSFCSRFIREVOERWALL 107
 Db 650 EKOKQPL-LSKD-----ENGLRWNF----DPALVRL-----LREV--KYFTLL 686

Qy 108 YDVISVSKLACQAMRQLHBAIAIQSKALFSKAEEQILSKVGSTSQFLETQFDLHLRHP 167
 Db 687 EQPV-----PESASILYSKN-----DTRE----- 706

Qy 168 DAFTYLARTAKALQAHWQLMKQYVYLEDQVQ-PLKPGQVL-----NFSDAEDLID 217
 Db 707 --YIVQOLEMIVENHNFTVQLHPMEFLPKNRKIEKMDDEVLKFGIEHYKWNSNDNPKIE 763

Qy 218 DSKLQKMDMDEVLHLMVADLRQKRKEIROLEQILHKW---QVLDSDTCGMSSDFDNCILA 275
 Db 764 TAKA-TVDEL--HOIV--OKMKETKLKIEALEKFENTKIKTERKONKPMSPDDYDQFLKA 816

Qy 276 VLGRGMRVYLMRSRBTITGRATED-NQIDVDSLLEGAW 313
 Db 817 VVQNKL--SIVKONGTSINKLVEWDYKVDKQQ-AW 852

RESULT 14

G6522 F11A17_16 [imported] - Arabidopsis thaliana
 C-Species: Arabidopsis thaliana (mouse-ear cress)
 C-Accession: G96522
 R-Theologis, A.; Becker, J.R.; Palm, C.J.; Federer, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.

A-Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, B.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A-Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A-Reference number: A66141; MUID:21016719; PMID:11130712
 A-Accession: G96522
 A-Status: preliminary
 A-Molecule type: DNA
 A-Residues: 1-558 <STO>
 A-Cross-references: GB:AE005173; NID:98778962; PLDN:AD49768.2; GSDB:GN00141
 C:Genetics:
 A:Gene: F11A17_16
 A:Map position: 1

Query Match 5.2%; Score 103.5; DB 2; Length 1825;
 Best Local Similarity 21.6%; Pred. No. 69; Mismatches 124; Indels 75; Gaps 15;
 Matches 71; Conservative 59; Mismatches 124; Indels 75; Gaps 15;

Qy 52 QPIQVTKDGLRKWPANDL-LINAVQTLNTLSVHLGVKSFCSRFIREVOQ----ERWYA 105
 Db 540 BEQOMKMLRAEW-GNDLPSVLQLETOQ- HIHTSVE-ELGSSVKEARLYGKMSQNFH 594

Qy 106 LIVDPVSKLACQ-----AMRQLRPEALIAIOSKA-----LFSKAEBULISKGST 151
 Db 595 TSVYETLGKLETQYCKLKETSSFRMRHLQSLHFKVSRATEELJWLNGKEEELACD-WSD 653

Qy 152 SQT-----LETQDL-----LHRHDAYLARTAKALQAHWQL 185
 Db 654 SNINPISAKKTYSELTMELLEGKODVERSLSQDPAEVISLNHAKOTVEAYSAVOSLOW 713

Qy 186 MKQYVYLEDQTVOPPLKGQDQVNFSADBLLDSDKLUKMRDVELEHMLVADRRO--KRE 243
 Db 714 MKOLCLCVCQHVKENAAVFQP--FSDARDL--ESFLRNQDSI--KRYTADRTSLSR 767

Qy 244 IROLEQELHKWQVWLSITGMSPDENOQTLAVTRGRMVYMRSR-----EI 291
 Db 768 EDLQDSDMDEKEQOLQSKSVSLSVGRSKTIVQKPRNPDHVLKSTLSVKAICDYRQEII 827

Qy 292 TIGRATKONQIDVDSLLEGPAWNSKRG 320
 Db 828 TI---CKNDECYLEDNSORTKWKVISPTG 833

Search completed: March 27, 2003, 05:22:44
 Job time : 57 sec

Qy 316 -----HNSIVGEI--QWPSAHLTIAKADIETKGEFI--NDLHQKVITC----- 355
 Db 274 AKQARAQKSP-----PVSQOLQINKQDNRSNLSQSYNGNKSQVNSA----- 315

Qy 103 WYALLYDYPVSKLACQAMRQLHPEAIA-IQSALKFLSKAEEQILSKVGSTSQFLETQFD 161
 Db 44 TKRVKSKQPLQYTKDGLGRWKPANDL-LINAVQTLNTLSVHLGVKSFCSRFIREVOER 102
 Db 214 VESSRSLSPSPSPSRRLPPTPPLPKFLVSPASSLQGRDENNSPPFPAPPPTPPPPPPL 273

Qy 356 ----- 218 -DSKLUKDRDR--VLEH--ELMVAADRROK---RETRQLEQELHKWQVLFVSDITGMSS 266

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GenCore version 5.1.4_P5_4578
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Om protein - protein search, using sw model

Run on:

March 27, 2003, 05:06:28 ; Search time 23 Seconds

(without alignments)

703.294 Million cell updates/sec

Title: perfect score: US-09-744-125A-2

Sequence: 1 NSARGVVEPGRCGSGSEPPSS.....LINQDLIALTRAEEKAKITPQ 390

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Result No. Score Query Length DB ID

Description

RESULT	ID	K122_STRPUR	STANDARD;	PRT;	699 AA.
1	K122_STRPUR	P46872	STRONGYLOCE	AC	P46872; (Rel. 32, Created)
2	K122_STRPUR	P46872	STRONGYLOCE	DT	01-NOV-1995 (Rel. 32, Last sequence update)
3	K122_STRPUR	P46872	STRONGYLOCE	DT	15-JUN-2002 (Rel. 41, Last annotation update)
4	K122_STRPUR	P46872	STRONGYLOCE	DE	Kinesin-II 85 kDa subunit (KRP85/95 85 kDa subunit).
5	K122_STRPUR	P46872	STRONGYLOCE	GN	KRP85.
6	K122_STRPUR	P46872	STRONGYLOCE	OS	Strongylocentrotus purpuratus (Purple sea urchin).
7	K122_STRPUR	P46872	STRONGYLOCE	OC	Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinidae; Euechinoidea; Benthinoidea; Echinacea; Echinoidea; Strongylocentrotidae; Strongylocentrotus.
8	K122_STRPUR	P46872	STRONGYLOCE	OC	OXB1_TAXID=7668;
9	K122_STRPUR	P46872	STRONGYLOCE	RN	[1]
10	K122_STRPUR	P46872	STRONGYLOCE	RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
11	K122_STRPUR	P46872	STRONGYLOCE	RC	TISSUE=Egg;
12	K122_STRPUR	P46872	STRONGYLOCE	RX	MEDLINE=94050179; PubMed=8232586;
13	K122_STRPUR	P46872	STRONGYLOCE	RA	Cole D.G., Chinn S.W., Wedaman K.P., Hall K., Vuong T., Scholey J.M.; "Novel heterotrimeric kinesin-related protein purified from sea urchin eggs"; Nature 356:268-270(1993).
14	K122_STRPUR	P46872	STRONGYLOCE	RA	-1- KINESIN-LIKE SUBUNITS OF 95 kDa (KRP95) AND 85 kDa (KRP85).
15	K122_STRPUR	P46872	STRONGYLOCE	CC	-1- KINESIN-LIKE SUBUNITS OF 95 kDa (KRP95) AND 85 kDa (KRP85).
16	K122_STRPUR	P46872	STRONGYLOCE	CC	-1- PTM: THE N-TERMINUS IS BLOCKED.
17	K122_STRPUR	P46872	STRONGYLOCE	CC	-1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
18	K122_STRPUR	P46872	STRONGYLOCE	CC	II SUBFAMILY.
19	K122_STRPUR	P46872	STRONGYLOCE	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
20	K122_STRPUR	P46872	STRONGYLOCE	CC	CC
21	K122_STRPUR	P46872	STRONGYLOCE	DR	EMBL; LJ6993; AAC16098.1, ...
22	K122_STRPUR	P46872	STRONGYLOCE	DR	HSPB; P17119; 3KR.
23	K122_STRPUR	P46872	STRONGYLOCE	DR	InterPro; IPR00152; kinesin_motor.
24	K122_STRPUR	P46872	STRONGYLOCE	DR	Pram; P00225; kinesin_1.
25	K122_STRPUR	P46872	STRONGYLOCE	DR	PRINTS; PR00380; KINESINHEAVY.
26	K122_STRPUR	P46872	STRONGYLOCE	DR	SMART; SM00129; KISC_1.
27	K122_STRPUR	P46872	STRONGYLOCE	DR	PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
28	K122_STRPUR	P46872	STRONGYLOCE	DR	PROSITE; PS00671; KINESIN_MOTOR_DOMAIN2; 1.
29	K122_STRPUR	P46872	STRONGYLOCE	KW	Motor protein; Microtubules; ATP-binding; Coiled coil.
30	K122_STRPUR	P46872	STRONGYLOCE	FT	DOMAIN 1 340 KINESIN-MOTOR (BY SIMILARITY).
31	K122_STRPUR	P46872	STRONGYLOCE	FT	DOMAIN 341 619 COILED COIL (BY SIMILARITY).
32	K122_STRPUR	P46872	STRONGYLOCE	FT	DOMAIN 620 699 GLOBULAR (BY SIMILARITY).
33	K122_STRPUR	P46872	STRONGYLOCE	FT	NP_BIND 97 104 ATP (POTENTIAL).
		SEQUENCE	699 AA;	SQ	78697 MW; 7B386611CB08190 CRC64;

ALIGNMENTS

001056 herpesvirus
 082839 rattus norv
 015078 homo sapien
 Q90512 fugu rubrip
 Q8781 archaeoglob
 002828 capra hircu
 P47591 mycoplasma
 P29172 bos taurus
 Q2824 chlamydia p
 Q66335 mus musculu
 Q28274 mycoplasma
 Q00274 mycoplasma

FT	REPEAT	740	824	SPECTRIN 2.
FT	REPEAT	837	930	SPECTRIN 3.
FT	REPEAT	1315	1415	SPECTRIN 4.
FT	DOMAIN	1469	2756	COILED COIL (POTENTIAL).
FT	REPEAT	2826	2863	PLECTIN 1.
FT	REPEAT	2864	2901	PLECTIN 2.
FT	REPEAT	2902	2939	PLECTIN 3.
FT	REPEAT	2940	2977	PLECTIN 4.
FT	REPEAT	2978	3015	PLECTIN 5.
FT	REPEAT	3116	3153	PLECTIN 6.
FT	REPEAT	3154	3191	PLECTIN 7.
FT	REPEAT	3192	3229	PLECTIN 8.
FT	REPEAT	3230	3267	PLECTIN 9.
FT	REPEAT	3268	3305	PLECTIN 10.
FT	REPEAT	3343	3380	PLECTIN 11.
FT	REPEAT	3522	3559	PLECTIN 12.
FT	REPEAT	3553	3560	PLECTIN 13.
FT	REPEAT	3561	3598	PLECTIN 14.
FT	REPEAT	3599	3636	PLECTIN 15.
FT	REPEAT	3640	3674	PLECTIN 16.
FT	REPEAT	3857	3895	PLECTIN 17.
FT	REPEAT	3898	3933	PLECTIN 18.
FT	REPEAT	3934	3971	PLECTIN 19.
FT	REPEAT	3975	4008	PLECTIN 20.
FT	REPEAT	4009	4100	PLECTIN 21.
FT	REPEAT	4101	4138	PLECTIN 22.
FT	REPEAT	4139	4176	PLECTIN 23.
FT	REPEAT	4177	4214	PLECTIN 24.
FT	REPEAT	4218	4252	PLECTIN 25.
FT	REPEAT	4265	4305	PLECTIN 26.
FT	REPEAT	4319	4356	PLECTIN 27.
FT	REPEAT	4445	4478	PLECTIN 28.
FT	REPEAT	4446	4483	PLECTIN 29.
FT	REPEAT	4484	4521	PLECTIN 30.
FT	REPEAT	4522	4559	PLECTIN 31.
FT	REPEAT	4560	4597	PLECTIN 32.
FT	DOMAIN	4250	4300	PLECTIN 33.
FT	VARSPPLIC	4625	4640	BINDING TO INTERMEDIATE FILAMENTS (BY SIMILARITY).
FT	MOD_RES	4539	4539	4 X 4 AA TANDEM REPEATS OF G-S-R-X. PHOSPHORYLATION (BY CDC2) (BY SIMILARITY).
FT	VARSPPLIC	1	174	MVAGMLMPDQLKAIYELFREGYUWAKKDRPRSLHPHP GVNLQVWMAASLURGIVRLFWCHFWLNGEHL ROYLHLPPVTAASLQRVPRYVAMMPARTPVAVOCPL GSPPRKGPAPTEFOLYRKELESEVSPEPFPVVAITORTIA RPGEPAPAT -> MSGDAEVRAVSDEVSUNGSGSPGDP TLPWNLQKWRSSRGGSNSVLDPAERAVIRIA (IN ISOFORM 2 AND ISOFORM 3). MISSING (IN ISOFORM 3). L -> LL (IN MD-EBI). /FTId=VAR_011336.
FT	VARIANT	1003	1005	MISSING (IN MD-EBI). /FTId=VAR_011337.
FT	CONFLICT	185	185	S -> F (IN REF. 2). N -> D (IN REF. 2). H -> N (IN REF. 2). I -> V (IN REF. 2). O -> R (IN REF. 2). N -> T (IN REF. 2). V -> A (IN REF. 2). V -> L (IN REF. 2). L -> V (IN REF. 2). V -> L (IN REF. 2). I -> M (IN REF. 2). A -> T (IN REF. 2). WLC -> RLR (IN REF. 2).
FT	CONFLICT	1309	1321	Q -> E (IN REF. 2). L -> A (IN REF. 2). K -> R (IN REF. 2). K -> N (IN REF. 2). S -> R (IN REF. 2). R -> Q (IN REF. 2).
FT	CONFLICT	1789	1910	SEQUENCE OF 1-497 FROM N.A.
FT	CONFLICT	1910	2154	SEQUENCE OF 1-497 FROM N.A.
FT	CONFLICT	2154	2160	SEQUENCE OF 1-497 FROM N.A.
FT	CONFLICT	2215	2221	SEQUENCE OF 1-497 FROM N.A.
FT	CONFICT	1767	1789	RX MEDLINE:8727512; PubMed:3607877;
FT	CONFICT	1789	1910	RX Davies K.E., Speer A., Billowitz H., Gross G.S., Forrest S.N., Koenig M., Hoffman E.P., Bertelson C.J., Monaco A.P., Reener C., Kunkel L.M.; "Two human cDNA molecules coding for the Duchenne muscular dystrophy (DMD) locus are highly homologous"; Nucleic Acids Res. 17:5391-5391(1989).
FT	CONFICT	1910	2154	"Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary genomic organization of the DMD gene in normal and

- RT affected individuals.";
- RL Cell 50:509-517(1987).
- RN [4]
- SEQUENCE OF 404-1137 FROM N.A.
- RX MEDLINE=8811512; PubMed=3428261;
- RA Cross G.S., Speer A., Rosenthal A., Forrest S.M., Smith T.J., Edwards Y., Flint T., Hill D., Davies K.E.;
- RT "Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystrophy patients.";
- RL EMBO J. 6:3277-3283 (1987).
- RN [5]
- SEQUENCE OF 655-722; 2058-2204 AND 2305-2366 FROM N.A.
- RX MEDLINE=89083552; PubMed=3205741;
- RA Chamberlain J.S., Gibbs R.A., Ranier J.A., Nguyen P.N., Caskey C.T.;
- RT "Deletion screening of the Duchenne muscular dystrophy locus via multiplex DNA amplification.";
- RL Nucleic Acids Res. 16:1141-1156(1988).
- RN [6]
- SEQUENCE OF 2147-2204 FROM N.A.
- RX MEDLINE=89345155; PubMed=2567720;
- RA Blonden L.J.T., den Dunnen J.T., van Paassen H.M.B., Bakker E., Wapenaar M.C., Grootenhuis P.M., Ginjaar H.B., Bakker E., Pearson P.L., van Ommen G.J.B.;
- RT "High resolution deletion breakpoint mapping in the DMD gene by whole cosmid hybridization.";
- RL Nucleic Acids Res. 17:5611-5621(1989).
- RN [7]
- SEQUENCE OF 2105-2164 FROM N.A.
- RA Huth A., Will K., Speer A., Bauer D., Submitted (MAR-1991) to the EMBL/GenBank/DBJ databases.
- RN [8]
- REVIEW ON DMD POINT MUTATION VARIANTS.
- RX MEDLINE=95038763; PubMed=795253;
- RA Roberts R.G., Gardner R.J., Bobrow M.;
- RT "Searching for the 1 in 2,400,000: a review of dystrophin gene point mutations";
- RT "Mutat. 4:1-11(1994).
- RN [1]
- REVIEW ON VARIANTS.
- RX MEDLINE=94320540; PubMed=8045556;
- RA Rintala R., Reiss J.;
- RT "Microlesions and polymorphisms in the Duchenne/Becker muscular dystrophy gene.";
- RL Hum. Genet. 94:111-116 (1994).
- RN [10]
- RP VARIANT DMD ARG-54.
- RX MEDLINE=9404652; PubMed=8401582;
- RA Prior T.W., Papp A.C., Snyder P.J., Burghes A.H.M., Bartolo C., Sedra M.S., Western L.M., Mendell J.R.;
- RT "A missense mutation in the dystrophin gene in a Duchenne muscular dystrophy patient.";
- RL Nat. Genet. 4:357-360(1993).
- RN [11]
- RP VARIANTS DMD HIS-365; TRP-2191 AND ARG-2937.
- RX MEDLINE=9515225; PubMed=7849724;
- RA Nigro V., Nigro G., Esposito M.G., Comi L.I., Molinari A.M., Puca G.A., Politan L.;
- RT "Novel small mutations along the DMD/BMP gene associated with different phenotypes.";
- RT "Hum. Mol. Genet. 3:1907-1908(1994).
- RN [12]
- RP ALTERNATIVE SPlicing (DYSTROPHIN-1 AND -2).
- RC TISSUE=Retina;
- RA White R.A.;
- RL Submitted (JAN-1995) to the EMBL/GenBank/DDJB databases.
- RN [13]
- RP ALTERNATIVE SPlicing (DYSTROPHIN-3).
- RC TISSUE=Brain;
- RA MEDLINE=89181947; PubMed=2648158;
- RA Feener C.A., Koenig M., Kunkel L.M.;
- RT "Alternative splicing of human dystrophin mRNA generates isoforms at the carboxy terminus.";
- RN
- RL Nature 338:509-511(1989).
- CC -!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE.
- CC -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPlicing; THE 3 SHORTER VARIANTS ARE CALLED DYSTROPHIN-1,-2 AND -3.
- CC DISEASE: Defects in DMD are the cause of Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD). DMD is the most common form of muscular dystrophy, a sex-linked recessive disorder. It typically presents in boys aged 3 to 7 year as proximal muscle weakness causing waddling gait, toe-walking, lordosis, frequent falls, and difficulty in standing up and climbing up stairs. The pelvic girdle is affected first, then the shoulder girdle. Progression is steady and most patients are confined to a wheelchair by age of 10 or 12. Flexion contractures and scoliosis ultimately occur. About 50% of patients have a lower IQ than their genetic expectations would suggest. There is no treatment. BMD resembles DMD in hereditary and clinical features but is later in onset and more benign.
- CC -!- DISEASE: Defects in DMD are a cause of X-linked dilated cardiomyopathy (XCM).
- CC IT IS 2.4 MILLION BASE-PAIRS IN SIZE AND COMPRISES 79 EXONS.
- CC -!- MISCELLANEOUS: THE DMD GENE IS THE LARGEST KNOWN GENE IN HUMANS.
- CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DISTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODIN).
- CC -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
- CC -!- SIMILARITY: CONTAINS 22 SPECTRIN REPEATS.
- CC -!- SIMILARITY: CONTAINS 1 WW DOMAIN.
- CC -!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
- CC -!- DATABASE: NAME=DMD; NOTE=Dystrophin Mutation Database; WWW=<http://www.dmd.nl/database.html>.
- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
- CC -----
- DR EMBL; X05179; CA39545.1; ALT_SEQ.
- DR EMBL; X06178; CA29544.1; ALT_SEQ.
- DR EMBL; X14298; CA3479.1; ALT_SEQ.
- DR EMBL; X15495; CA33518.1; --.
- DR EMBL; X56820; CA38589.1; --.
- DR EMBL; X13045; CA31451.1; --.
- DR EMBL; X13046; CA31452.1; --.
- DR EMBL; X13047; CA31453.1; --.
- DR EMBL; X13048; CA31454.1; --.
- DR EMBL; U07203; AA86115.1; --.
- DR EMBL; U21203; AA86116.1; --.
- DR EMBL; X15148; CA33245.1; --.
- DR PIR; A27605; A27605.
- DR PIR; A27162; A27162.
- DR PIR; S05291; S05291.
- DR HSSP; P46939; 1QAG.
- DR GeneW; HGNC:2228; DMD.
- DR MIM; 300377; --.
- DR MIM; 310200; --.
- DR MIM; 300376; --.
- DR MIM; 302045; --.
- DR InterPro; IPR01589; Actbind_actnln.
- DR InterPro; IPR01715; Calponin-like.
- DR InterPro; IPR02017; Spectrin.
- DR InterPro; IPR01202; WW_Rsp5_WWP.
- DR InterPro; IPR00433; Znf_ZZ.
- DR InterPro; IPR00307; CH; 2.
- DR Pfam; PF00397; WW; 1.
- DR Pfam; PF00435; spectrin; 22.
- DR Pfam; PF00569; ZF; 1.
- DR PRINTS; PR00403; WDdomain.

PT DOMAIN 134 237 CH 2.
 PT REPEAT 341 449 SPECTRIN 1.
 PT REPEAT 450 558 SPECTRIN 2.
 PT REPEAT 561 669 SPECTRIN 3.
 PT REPEAT 721 830 SPECTRIN 4.
 PT REPEAT 832 936 SPECTRIN 5.
 PT REPEAT 945 1047 SPECTRIN 6.
 PT REPEAT 1050 1156 SPECTRIN 7.
 PT REPEAT 1159 1265 SPECTRIN 8.
 PT REPEAT 1268 1369 SPECTRIN 9.
 PT REPEAT 1470 1570 SPECTRIN 10.
 PT REPEAT 1573 1678 SPECTRIN 11.
 PT REPEAT 1681 1782 SPECTRIN 12.
 PT REPEAT 1879 1981 SPECTRIN 13.
 PT REPEAT 2013 2103 SPECTRIN 14.
 PT REPEAT 2106 2210 SPECTRIN 15.
 PT REPEAT 2213 2318 SPECTRIN 16.
 PT REPEAT 2468 2570 SPECTRIN 17.
 PT REPEAT 2573 2679 SPECTRIN 18.
 PT REPEAT 2682 2795 SPECTRIN 19.
 PT REPEAT 2798 2900 SPECTRIN 20.
 PT REPEAT 2902 2924 SPECTRIN 21.
 PT REPEAT 2927 3033 SPECTRIN 22.
 PT DOMAIN 3048 3081 WW.
 PT ZN_FING 3300 3347 2Z-TYPE.
 PT CONFLICT 463 463 D -> H (IN REF. 3).
 PT CONFLICT 677 677 S -> F (IN REF. 3).
 PT CONFLICT 2337 2337 V -> L (IN REF. 1; AAB02797).
 SQ AA; 425810 MN; 1D2E74CP7DB035EE CRC64;

Query Match 5.1%; Score 102; DB 1; Length 3678;
 Best Local Similarity 20.9%; Pred. No. 75; Matches 69; Conservative 60; Mismatches 121; Indels 80; Gaps 14;
 FT CONFLICT 3678 AA;

QY 3.2 PVPPEPAPAGLTKRKVKKSQPLQVTKDGRWKPAANDLLINAVIQTNDLTSVHGVKFS 91
 3410 PVDSAPASSPQLSHDTHSRIEHVIAKR-LAEMENNSGNSYLNDSISPNEISIDDEHILLIQHY 3468

Db 92 CRFTIREVQERWYALIYDPVISKLACQAMHQMLQHPIAAIQSKALKSKAEQOLISKVGST 151
 QY 3469 CQ-----SLNQDPLSQ----PRSPAQILSLESE 3494

QY 152 SQPTE-TFQDLHLRRHPDAFYLTAKALQAHQWLMKQYVILEDDQTQVQPLPKGPQVQVLNFs 210
 Db 3495 ERGEELRLIADLEEN-----RNQAEYDPLKQH--ERHGCLSPPLSPPEMMPS 3542

QY 211 -----DAEDLDDSKLKDMDRDEVILHELMYADRRQKRETROOLEDTLHKWQVLD----- 259
 Db 3543 PQSPRDAE-TIAEAUJLROHKGRJLARMQILEDHNK---QLESQHRLRQLQIPQPQAEA 3557

QY 260 --STRGMSSPDFFDNGTAVLRGRMRYLMSREITLGRATKDNOUDVDSLLEGAWKISR 317
 Db 3598 KVNGTIVSSPSTSLSRSDSSQPLMR-----WVGSQTSSESMGEEDL-LSPPODTSTG 3648

QY 318 KQGVVKLKNNGDPPFANEGRPIYIDGRPV 347
 Db 3649 LEEVWQLNNS--FSSRGFM--APGKPM 3673

RESULT 7
 POL_CAEVC ID POL_CAEVC STANDARD; PRT; 1109 AA.

PT REPEAT 01-FEB-1994 (rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

PT REVERSE transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
 OS Caprine arthritis encephalitis virus (strain Cork) (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11661; OX [1]

SEQUENCE FROM N.A. RQ
 MEDLINE=91021037; PubMed=2171210;
 RX Saltarelli M., Querat G., Konigs D.A.M., Clements J.E.;
 RA "Nucleotide sequence and transcriptional analysis of molecular clones
 RT of CAEV which generate infectious virus.";
 RL Virology 179:347-344(1990);
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
 phosphomonooester.
 CC -!- CATALYTIC ACTIVITY: N deoxyribonucleoside triphosphate = N diphosphate
 CC + (DNA) (N).
 CC -!- PMT: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -!- MISCELLANEOUS: THIS PROTEIN MAY BE SYNTHESIZED AS A GAG-POL
 CC POLYPROTEIN.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
 KNOWN AS THE RETROPEPSIN FAMILY.
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CC EMBL; M33677; AA91826.1; ALT_INIT.
 DR PIR; B45345; B45345.
 DR HSSP; P16088; 1DUT.
 DR MEROPS; A02.006; .
 DR InterPro; IPR0011995; Asparto-protease_rtrv.
 DR InterPro; IPR0011969; Asparto-protease site.
 DR InterPro; IPR0011969; Asparto-protease_rtrv.
 DR InterPro; IPR01428; DeoxyUtpase.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR003308; Integrase_Zn.
 DR InterPro; IPR02156; RNaseH.
 DR InterPro; IPR00477; RNase.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00075; lnsash; 1.
 DR Pfam; PF00077; rvp; 1.
 DR Pfam; PF00078; rvt; 1.
 DR PROSITE; PS00141; ASP_Protease; 1.
 DR PROSITE; PS00175; ASP_Prot_RETROV; 1.
 KW Hydrolase; Aspartyl protease; RNA-directed DNA polymerase;
 KW Transferase; Nuclese; Endonuclease; Polyprotein.
 FT CHAIN 1 152 Aspartyl protease; Reverse transcriptase.
 FT CHAIN 153 865 Aspartyl protease; Reverse transcriptase.
 FT ACT SITE 866 1109 BY SIMILARITY.
 SQ SEQUENCE 1109 AA; 127678 MN; 97B2F4B370B03CF3 CRC64;

Query Match 5.1%; Score 101.5; DB 1; Length 1109;
 Best Local Similarity 19.7%; Pred. No. 16; Matches 81; Conservative 54; Mismatches 142; Indels 135; Gaps 20;

QY 21 EKKKVKSKAP----STPVPPSAPAPGLTKRKVKKSQPLQVTKDGRWKPAANDLLINAV 75
 Db 190 EGCKGKAPPWTCTNPi-----FCIKKKGKNEMLIDPRELNK- 228

QY 76 LQTNDLTSVH-----GVKFSCRTLREVOERNWALIYDPVISKLACQAMRQHPEAI 128
 Db 229 -QTEDLTLAQLGLPHGGGLQKKHVIILDIGDAYFTIPLYEP-YREYICFTL--LSPNML 284

QY 129 AAIOSKALSKAERQSLSKVGSISQPTL-EFCQDLHRP----- 168
 Db 285 G--PCKRYWVVLPOGWKLSPSVYQFTMOBILEDWIQQHPEIOPFGIYMDIYIGSDLETK 342

QY 169 -----AFYLA-----RTAKALQAH--QLMQYVILEDDQTQVQPLPKGDQVl 207
 Db 343 KHREITVKDLANYIAQYGFTLUPEEKRQGYPAKWLGFELHPTQWFKQKHTLPBLTKTITL 402

QY 208 NFSDAEIDLDDSKLKDMDDEVLEHE-----LNAVDRRQKRPIROLEQELHKWQ 255
 Db 403 N-----KLUQKLVGELVRQSLIGKSIPNLKUMGERELQSRRKIBEVHKEWE 451
 QY 256 VLVDSITGMSSPFDNQTLAVLRGGRMVRFLMRERETILGRATKDNQIDVLSLE-GPAW 313
 Db 452 ACRKKLEEMEG-----NYNKDKVYQOLAWGDKA1EYIVYQEKGPWL 495
 QY 314 -----KISRKGQVTKLNN-GDFFIKANEGRP-IYIDGRLVLCGSKWRL 355
 Db 496 VNVVHNIKNLSTIQQVTKAQLK-TQEVTRTGSKIPWILLPGKE---EDWRL 543

RESULT 8

DMD_CANFA	STANDARD;	PRT;	3680 AA.
ID DMD_CANFA			
AC 037592;			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DB Dystrophin.			
GN DMD.			
OS Canis familiaris (Dog)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
RN [1]			
RP STRAIN=golden retriever;			
RA Carville K.S., Mann C.J., Schatzberg S.J., Wilton S.D.;			
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.			
CC --!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE.			
CC --!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODIN).			
CC --!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.			
CC --!- SIMILARITY: CONTAINS 22 SPECTRIN REPEATS.			
CC --!- SIMILARITY: CONTAINS 1 WW DOMAIN.			
CC --!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.			

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EMBL: AP070485; AAC83646.1; -
 HSPB; P46939; 1QAG
 InterPro: IPR001589; Actbind_actinin.
 DR InterPro: IPR001715;
 DR InterPro: IPR002017; Spectrin.
 DR InterPro: IPR002020; WW_Rps5_WWP.
 DR InterPro: IPR00433; ZnF_ZZ.
 DR Pfam: PF00077; CH_2.
 DR Pfam: PF00397; WW_1.
 DR Pfam: PF00435; spectrin_21.
 DR Pfam: PF00569; ZZ_1.
 DR SMART; SNO0150; SPIC; 21.
 DR SMART; SNO0456; WW_1.
 DR SMART; SNO0291; Znf_ZZ; 1.
 DR PROSITE; PS00019; ACTININ_1; 1.
 PROSITE; PS00020; ACTININ_2; 1.
 PROSITE; PS50021; CH_2.
 PROSITE; PS00159; WW_DOMAIN_1; 1.
 PROSITE; PS50020; WW_DOMAIN_2; 1.
 PROSITE; PS01357; ZF_ZZ_1; 1.
 PROSITE; PS50135; ZF_ZZ_2; 1.
 KW Repeat; Zinc-finger.
 FT DOMAIN 15 119
 FT DOMAIN 134 237
 FT REPEAT 340 448
 FT REPEAT 449 557
 FT REPEAT 560 668
 FT REPEAT 720 829
 FT REPEAT 831 935
 FT REPEAT 944 1047
 FT REPEAT 1050 1155
 FT REPEAT 1159 1265
 FT REPEAT 1268 1369
 FT REPEAT 1470 1570
 FT REPEAT 1573 1678
 FT REPEAT 1782 1879
 FT REPEAT 1879 2103
 FT REPEAT 2106 2210
 FT REPEAT 2213 2320
 FT REPEAT 2470 2572
 FT REPEAT 2575 2681
 FT REPEAT 2684 2797
 FT REPEAT 2800 2902
 FT REPEAT 2904 2926
 FT REPEAT 2929 3035
 FT DOMAIN 3050 3083
 FT ZN_FING 3302 3349
 SQ SEQUENCE 3680 AA; 425650 MW; 539FC9D72377072 CRC64;

Query Match 5.1%; Score 101; DB 1; Length 3680;
 Best Local Similarity 22.8%; Pred. No. 89; Matches 83; Indels 101; Gaps 15;
 Matches 66; Conservative 40; Mismatches 83; Indels 101; Gaps 15;

QY 16 EPSSSEKVKVSKAPSTPPSPAPAGT----KRVKESKQPLQVTKDGRWK--P 65
 Db 2399 EDISSLWKVNTQDLOLQEAKOQCPGAPGTTVAPPSCPTVLTQDPT-AVTKETAIKSLMP 2457

QY 66 ANDILLINAVLQTN---DLTSVHLGVFKSCRFTRREVQERNVALLYDPVI----- 112
 Db 2458 SSILLEVALDENRAWMELTD-----WNUU-DRVILQRQVMWD 2497

QY 113 -----SLKACQAMRQLPPEATAIAIOSKALFSKAEQOLISKVQESTSQTLFQDL 162
 Db 2498 LEDINEMITKQKATLQDLEQRPOLELL-----TAQNQKNTISQEARVITIT-DR 2548

QY 163 LHRHPDAYLARITAKAQLAHWQLMKQYY-----LLEDQT-VQLPKDQVQIWFSD 211
 Db 2549 IER-----IQSONWVQEHQNLQRQLQITEMKQDTSWLAKEERABQVLGQAR 2595

QY 212 AEDLIDDSKIKMDDEVLEHELNADVRQKR-EIROQEELHKWQVLVD 259
 Db 2596 A-----KLESMKEAR-----YTVDIAQKKITETQQLAKDURQWQINV 2633

RESULT 9

SYS_MYCGE	STANDARD;	PRT;	417 AA.
ID SYS_MYCGE			
AC P47251;			
DT 01-FEB-1996 (Rel. 33, Created)			
DT 01-FEB-1996 (Rel. 33, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE SerrT-tRNA synthetase (EC 6.1.1.11) (Serine-tRNA ligase) (SerrRS)			
DR SERS OR MG005.			
OS Mycoplasma genitalium.			
DR Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX NCBI_TaxID=2097; [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 33530 / G-37;			
RX MEDLINE-9620346; Pubmed=769993;			
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,			

Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;

RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchinson C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.", Science 270:337-403(1995).

RA [2] SEQUENCE OF 1-125 FROM N.A.

RP STRAIN=ATCC 33530 / G-37;

RC MEDLINE=94364962; PubMed=8083173;

RA Bailey C.C., Bott K.F.;

RT "An unusual gene containing a dnaJ N-terminal box flanks the putative origin of replication of Mycoplasma genitalium.", J. Bacteriol. 176:5814-5819(1994).

RN [3] SEQUENCE OF 6-11 FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=94075230; PubMed=8253680;

RA Peterson S.N., Hu P.-C., Bott K.F., Hutchinson C.A. III; "A survey of the Mycoplasma genitalium genome by using random sequencing.", J. Bacteriol. 175:7918-7930(1993).

RT CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate + L-seryl-tRNA(Ser).

CC SUBUNIT: HOMODIMER (BY SIMILARITY).

CC SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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CC

DR EMBL; U39879; AACT1221.1; -.

DR EMBL; U09551; AA5073.1; -.

DR EMBL; U02210; AAD12502.1; -.

DR HSSP; P34945; 1SER.

DR MG005; -.

DR TIGR; MG005; -.

DR InterPro; IPR002106; AATRNA_ligaseII.

DR InterPro; IPR002314; tRNA-synth_2b.

DR InterPro; IPR002317; tRNA-synth_2b.

DR Pfam; PF00587; tRNA_synt_2b; 1.

DR Pfam; PF02403; Seryl_tRNA_N; 1.

DR PRINTS; PR00981; TRNA_SYNTHESER.

DR TIGR4MS; TIGR00414; sers; 1.

DR PROSITE; PS5082; AA_TRNA_LIGASE_IT; 1.

KW Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 417 AA; 47987 MW; 5E43280A5915DD0 CRC64;

Query Match 5.0%; Score 99.5; DB 1; Length 417; Best Local Similarity 23.2%; Pred No 57; Mismatches 41; Conservative 35; MisMatches 62; Indels 39; Gaps 8; Matches 41; Gaps 8;

Qy 215 LIDPSKLKDMD-----SYLEHEMWARRRKKRETRQRLKQWVQVDSIT 262

Db 1 MLDPKNLRRNNYDFFKKKLLERNVNROLLNPIOTDKLMRKNLQQBLANQKSLAKQVA 60

Qy 263 GMSSSDPDNQTLAVIRGRGMWRYLMMSREI-----TGRATKNDQ-IDVDSLEGPAWKIS 316

Db 61 KQK-----DNKEL-----LASPKELKQKIELNNAVAKDSQDQNLINFP--NIA 104

Qy 317 RKQGVYKLKNGDFIANGNEGRPVTIDGRPV---LCGSKWRLSHNSVVEASIFPV 369

Db 105 HESVPVGKNESENLSLLKEGRKPFV-DFKPLPHRELCEKUNLVADKATISKGTFV 160

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DB 1-aminocyclopropane-2-carboxylate synthase 2 (EC 4.4.1.14) (ACC synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase 2).

GN ACS2 OR ATG01480 OR F2214.4.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_TaxID=3702;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RC MEDLINE=93028584; PubMed=1357670;

RA van der Straeten D., Rodrigues-Pousada R.A., Villarroel R., Hanley S., Goodman H.M., van Montagu M.;

RT "Cloning, genetic mapping, and expression analysis of an Arabidopsis thaliana gene that encodes a 1-aminocyclopropane-1-carboxylate synthase.", Proc. Natl. Acad. Sci. U.S.A. 89:9969-9973 (1992).

RN [2] SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RC MEDLINE=93066381; PubMed=1433312;

RA Liang X.-W., Abel S., Keller J.A., Shen N.F., Theologis A.;

RT "The 1-aminocyclopropane-1-carboxylate synthase gene family of Arabidopsis thaliana.", Proc. Natl. Acad. Sci. U.S.A. 89:11046-11050(1992).

RN [3] SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RA Terry N.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

RN [4] SEQUENCE FROM N.A.

RP STRAIN=cv. Columbia;

RC MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Becker J.R., Palm C.J., Fedderspiel N.A., Kaul S., White O., Alonso J., Altafai H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H.H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway T.H., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzdar L., RA Hunter J.L., Jenkins J., Haas B., Hansen N.F., Hughes B., Huzdar L., Kim C.J., Koo H.I., Kremetskaya I., Kurtz D.B., Kwan A., Lam B., RA Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P., RA Lin X., Liu S.X., Liu Z.A., Luos J.S., Maiji R., Marziali A., RA Miltzschner J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I., RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M., RA Sun H., Tallon L.J., Tambungua G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysockaia V.S., Walker M., RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W., RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.", Nature 408:816-820(2000).

RT Nature 408:816-820(2000).

CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.

CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 1-aminoacylcopropane-1-carboxylate + methythioadenosine.

CC -!- COFACTOR: Pyridoxal PHOSPHATE.

CC -!- PATHWAY: Ethylene biosynthesis; first (rate limiting) step.

CC -!- SUBUNIT: HOMODIMER.

CC -!- TISSUE SPECIFICITY: HIGH IN DEVELOPING LEAVES AND IN FLOWERS.

CC -!- INDUCTION: BY ETHYLENE.

CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

CC

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CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

RT "an *Arabidopsis* heat shock protein complements a thermotolerance defect in yeast."; Plant Cell 6:1899-1909(1994).
 RT [2]

CC SEQUENCE FROM N.A.

DR MEDLINE=20226114; PubMed=10760305;

RA Hong S.-W.; Viertling B.; *thaliana* defective in the acquisition of "Mutants of *Arabidopsis* tolerance to high temperature stress."; Proc. Natl. Acad. Sci. U.S.A. 97:4392-4397(2000).
 RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN=CV; Columbia;

DR MEDLINE=21016719; PubMed=1113012;

RA Theologis A.; Ecker J.R.; Palm C.J.; Pederspiel N.A.; Kaul S.' White O.; Alonso J.; Altafi H.; Araujo R.; Bowman C.L.; Brooks S.Y.; Pfam: PF00155; amiotran 1.2; 1.

DR PRINTS; PR0073; ACSYNTASE.

DR PROSITE; PS00105; AA_TRANSFER_CLASS 1; 1.

DR FRUIT ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate; Multi-gene family; Pyridoxal phosphate (BY SIMILARITY).

FT BINING 279 279

FT VARIANT 136 136 M → T.

FT SEQUENCE 496 AA; 55531 MW; 766318AE85F166 CRC64;

Qy Best Match 5.0%; Score 99.5%; DB 1; Length 496;
 Matches 68; Conservative 56; Mismatches 117; Indels 95; Gaps 12;

Qy 32 PVPSPSPAPAGLTK---RVTKSQPLQVTKDGRWKPAANDLLNAVQTNDLTSVHL 86

Qy 87 GVFKFSCRFTRREVQERWALY---DPVISKLAQAMRQLHEATAIKSKALFSKAEP 142

Db 225 -VRFVTRKNTLHVWVBIYAVTFAGGDFV-----SVAEVNDVSEVN 268

Qy 143 QLLSKVGSTSQP-----TLETFQDL---HRHPDAFVIAARTAKALQHWAQMOKYY 190

Db 269 DLHIVYLSKDMGLPGRFVRIVSFDNSVSCARKMSSFGI-----VSSQTOQMLASH 322

Qy 191 LLEDQTWQPIPKGDQVLNFSQDAEDLDDSKLKDMDREBVLHELMVAD----- 237

Db 323 LSDDGPFV-----NF-----LNESSRRRLGIRHKVFUTGKIKADIACLTSNAGLFAN 368

Qy 238 ---RQRQREIROLEQFLHKMVKVOLVLSITGMSP-----DFDNQTLAVL 277

Db 369 MDLRHILDRNSFESBIEILWHIIIDRKVKNVSPGSSPRCIEPGWMFRICFAANDDTLHVA 428

Qy 278 RGRMVTYLMSSREITGRATEKQDVIDLSLEGPAW 313

Db 429 LGRIODFVSKNNKTVKEASENDQVIONKSAAKKLNW 464

RESULT 11

H101_ARATH ID H101_ARATH STANDARD; PRT; 911 AA.

DT 01-Nov-1995 (Rel. 32; Created)
 DT 15-Jun-2002 (Rel. 41; Last sequence update)
 DT 15-Jun-2002 (Rel. 41; Last annotation update)

DE Heat shock protein 101.

GN HSP10 OR ATIG4310 OR F1017.2.

OS *Arabidopsis thaliana* (Mouse-ear cress).

OC Eukaryota; Viridiplanteae; Streptophytida; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II; Brassicidae; Brassicaceae; Arabidopsis; OC NCBI_TAXID=3702;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=CV; Columbia; TISSUE=Leaf; MEDLINE=95170291; PubMed=7866032; Schimmen E.C., Lindquist S., Vierling E.;

DR EMBL; M9559; AAA97516.1; -.

DR EMBL; Y12776; CAA7310.1; -.

DR EMBL; AC061957; AAF81308.1; -.

DR PIR; S31646; S31646.

DR PIR; A47199; A47199.

DR PIR; S46190; S46190.

DR HSSP; P37821; IBBG.

DR InterPro; IPR001176; ACC synthase.

DR InterPro; IPR004839; Aminotransf1.

DR InterPro; IPR004838; NHTtransf_1.

DR Pfam; PF00155; amiotran 1.2; 1.

DR PRINTS; PR0073; ACSYNTASE.

DR PROSITE; PS00105; AA_TRANSFER_CLASS 1; 1.

DR FRUIT ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate; Multi-gene family; Pyridoxal phosphate (BY SIMILARITY).

FT BINING 279 279

FT VARIANT 136 136 M → T.

FT SEQUENCE 496 AA; 55531 MW; 766318AE85F166 CRC64;

Qy Best Match 5.0%; Score 99.5%; DB 1; Length 496;
 Matches 68; Conservative 56; Mismatches 117; Indels 95; Gaps 12;

Qy 32 PVPSPSPAPAGLTK---RVTKSQPLQVTKDGRWKPAANDLLNAVQTNDLTSVHL 86

Qy 87 GVFKFSCRFTRREVQERWALY---DPVISKLAQAMRQLHEATAIKSKALFSKAEP 142

Db 225 -VRFVTRKNTLHVWVBIYAVTFAGGDFV-----SVAEVNDVSEVN 268

Qy 143 QLLSKVGSTSQP-----TLETFQDL---HRHPDAFVIAARTAKALQHWAQMOKYY 190

Db 269 DLHIVYLSKDMGLPGRFVRIVSFDNSVSCARKMSSFGI-----VSSQTOQMLASH 322

Qy 191 LLEDQTWQPIPKGDQVLNFSQDAEDLDDSKLKDMDREBVLHELMVAD----- 237

Db 323 LSDDGPFV-----NF-----LNESSRRRLGIRHKVFUTGKIKADIACLTSNAGLFAN 368

Qy 238 ---RQRQREIROLEQFLHKMVKVOLVLSITGMSP-----DFDNQTLAVL 277

Db 369 MDLRHILDRNSFESBIEILWHIIIDRKVKNVSPGSSPRCIEPGWMFRICFAANDDTLHVA 428

Qy 278 RGRMVTYLMSSREITGRATEKQDVIDLSLEGPAW 313

Db 429 LGRIODFVSKNNKTVKEASENDQVIONKSAAKKLNW 464

RP SEQUENCE OF 1-460 FROM N.A.

RC STRAIN=CV; Columbia;

RA Shinzaki K.; Davis R.W.; Ecker J.R.; Theologis A.; sequenced by the Swiss *Arabidopsis* full length cDNA clones (RAFLs).

RT SSP consortium (Salk/Stanford/FGEC).;

RL Submitted (Nov-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THERMOTOLERANCE.

CC -!- INDUCTION: BY HEAT SHOCK.

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CC DR EMBL; U13949; AAA67927.1; -.

CC DR EMBL; AF218796; AAF2423.1; -.

CC DR EMBL; AC020579; AAG5410.1; -.

CC DR EMBL; AY06259; AAL32674.1; -.

CC DR InterPro; IPR003593; AAA_APtpase.

CC DR InterPro; IPR003595; AAA_APtpase_cTPA/B.

CC DR InterPro; IPR004176; CIP_N.

CC DR Pfam; PF0004; AAA; 2.

CC DR Pfam; PF0081; CIP_N.

CC DR PRINTS; PR00300; CIPPROTEASE.

CC DR PRODOM; PD000739; GSPT1_E; 1.

CC DR SMART; SM00382; AAA; 2.

CC DR PROSITE; PS00870; CLPBP_1; 1.

CC DR PROSITE; PS00871; CLPBP_2; 1.

CC FT Chaperone; Heat shock; ATP-binding; Repeat.

CC FT DOMAIN 164 410 I.

CC FT DOMAIN 532 723 I.I.

CC FT DOMAIN 207 214 ATP (POTENTIAL).

CC FT NP-BIND 606 613 ATP (POTENTIAL).

CC or send an email to license@isb-sib.ch).

EMBL; S61883; AAB6991.2; -.

DR HSSP; Q92811; 1B91.

DR TRANSFAC; T02119; -.

DR Flybase; FBgn0010355; Taf250.

DR InterPro; IPR00637; AT_hook.

DR InterPro; IPR01487; Bromodomain.

DR InterPro; IPR01878; Znf_CCHC.

DR pfam; PF0043; bromodomain; 2.

DR Pfam; PF02178; AT_hook; 1.

DR PRINTS; PR0503; BRDMODOMAIN.

DR SMART; SW0384; AT_hook; 1.

DR SMART; SW0297; BRMO; 2.

DR PROSITE; PS0633; BRDMODOMAIN_1; 2.

DR PROSITE; PS50014; BRDMODOMAIN_2; 2.

KW Bromodomain; Nuclear Protein-DNA-binding; Cell cycle; Repeat; Transcription regulation; Phosphorylation.

FT DNA_BIND 1247 1360 HMG BOX (POTENTIAL).

FT DOMAIN 1451 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 1490 1560 BRDMODOMAIN_1.

FT DOMAIN 1612 1682 BRDMODOMAIN_2.

FT DOMAIN 1995 2068 GLN-RICH.

FT VARIANT 575 575 P > S.

SO SEQUENCE 2068 AA; 232494 MW; AD6A5ABF2B859531 CRC64;

Query Match 5.0%; Score 99.5%; DB 1; Length 2068;

Best Local Similarity 21.5%; Pred. No. 51; Mismatches 100; Indels 97; Gaps 15;

Matches 68; Conservative 51; MisMatches 100; Indels 97; Gaps 15;

QY 5 GGVEGRCS-----GSEPPSEKKVSKAASITPVPSA-----PAPGTTKRVKSK 51

Db 1000 GPADPTGCGGFFSTVRVPNPKPTQKEEQBSQ PKRSVYGTADIRRPLQRAKELLQRFK 1058

QY 52 QPLQTKDGRWKFLNDLILNATIQLTNDLTSVHLGV-KFS-CRFTRREVWRWALLY 108

Db 1059 VPEEIKKLRSW---EVIDVVRTLISTERAKAGBEGMDKFSRGNRFSIAHQERY---- 1109

QY 109 DPVSKLAQAMRQHPEALAIQ---SKALFSKAEBOLLKVG----- 149

Db 1110 -----KECORIFDQLQNRYLASSAEEVSLVSTDAAESSASBESDLEBLKGNNLENMLSNKKTSTQ 1164

QY 150 -STSTOPTEFLFDQI-----HRHDARYPLARTAKAQAHWQM----- 186

Db 1165 LSREBEELER-QELIRQLDEEHGGPGSGGGAKGKGDKDPGQMLATINQNQGRILRTRF 1223

QY 187 -----KOYIILEDQTYQPKGQDVLNFNSDAEDLIDDSKLKMRDEVYLEHELMVADRO- 240

Db 1224 RGNDEKEYTARVE--TVRQPOVIDAYI-----KRTTKDEQFIQKFAITDEQK 1269

QY 241 ---KREIROLQEELHK 253

Db 1270 EEMKKEKRRIIQEQLRR 1285

RESULT 13

PYRL_SCHPO	PYRL_SCHPO	STANDARD	PRT	2244 AA.
ID 009754;				
DT 01-NOV-1995 (Rel. 32, created)				
DT 01-Nov-1995 (Rel. 32, last sequence update)				
DT 15-JUN-2002 (Rel. 41, last annotation update)				
DE URA1 protein [includes: Glutamine-dependent carbamoyl-phosphate synthetase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2)].				
OS Schizosaccharomyces pombe (Fission yeast).				
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;				
OC Schizosaccharomycetales; Schizosaccharomycetaceae;				
OC Schizosaccharomycetes.				
NCBI_TaxID=4896;				
[1]				

SEQUENCE OF 22-2244 FROM N.A.

RN RP

Db 2202 NREIS-----EEVDFF 2212
 ID P70755;
 MUTS_AQUPY STANDARD; PRT; 855 AA.
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE DNA mismatch repair protein muts.
 DR
 OS Aquifex pyrophilus.
 RT "Hyperthermophilic Muts proteins: isolation, characterization and enhancement of CCR specificity."
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC
 [1] -!- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a weak ATPase activity (BY similarity).
 --!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
 CC
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 CC
 DR EMBL; U71154; AAB1998-1; -
 DR InterPro; IPR00432; MutS_C.
 DR IPRO02863; MutS_N.
 DR Pfam; PF01624; MutS_N; 1.
 DR ProDom; PDO01463; MutS_C; 1.
 DR SMART; SM00532; MutSd; 1.
 DR TIGRFAMS; TIGR01070; muts_1.
 DR PS0086; DNA_MISMATCH_REPAIR_2; 1.
 KW DNA repair; ATP-binding; DNA binding.
 FT NP BIND 607 614
 SEQUENCE 855 AA; 9765 MW; 5A8C8EBE23.E8A CRC64;
 Query Match 4.9%; Score 98.5; DB 1; Length 855;
 Best Local Similarity 21.4%; Preo. No. 18;
 Matches 83; Conservative 60; Mismatches 133; Indels 111; Gaps 18;
 QY 24 KVSKAPSTPPSPSP--APGLTKVVKSKPQLOPTKDL--GRWKPAANDLILAVLQTND 80
 DR 236 KATQFSFTPLPKPKPYDGGVYKUDLKAVKGLETESTEGR---KDLSLFKVW---D 287
 QY 81 LTSFLVGVKVFSCRFI-----REVOERWALLYDPVISKACQAMQLHPEAIA 130
 DR 288 RTRLGNG-RRRLREFLNPERSIEKRIVQE-----AVERLINK-----REVINE 331
 Db 190 YLLEDOTVOLPKGQVQLNSDAEDLUDPSKLKDRDEVEHELVNV---ADRIQKREIR 245
 QY 131 TOSKALFSKAE-EQILSKVGSTSQTPLETQDILKLRHPDAFYLTAKALQAHWQMLKQY 189
 DR 332 IR-KTLEGMSDLERLYSRSS---ANMASPRELH-----LNNSLRKAELRKIL 376
 QY 246 Q-LSEBLHKQVLVPSITGMSS-----PDF-DNQTLAVLRG 279
 DR 435 ENAEKLUKEKEKKKETGQSLKIGYKNGYYTEVKANKVYPERHFRROTLSAER 494
 DR
 QY 280 RMVYLMRSREITIGRATKDNQIDVL-----SLEGAWS 313
 DR 495 YTTEELQRKEEKIQLSAQRINNELEYRELREEVVKELDKVNNATLIGEVDYIQS LAW 594
 QY 314 KISRQGVVKLUNGDFFTANGRPI 340
 DR 555 LALEKGWVKEPVHEGYELIEEGKHPV 581
 QY 315 DYH9_HUMAN STANDARD; PRT; 4486 AA.
 DR DYH9_HUMAN 09NC9; 09NQ28; 095494;
 DR 16-OCT-2001 (Rel. 40, Created)
 DR 16-OCT-2001 (Rel. 40, Last sequence update)
 DR 16-OCT-2001 (Rel. 40, Last annotation update)
 DR Ciliary dynein heavy chain (Axonemal dynein heavy chain) (Dynein heavy chain 9)
 RN GN DNAH9 OR DNAH7L OR DNAL1.
 RN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteraria; Primates; Catarrini; Hominidae; Homo.
 CC NCB1-TaxID=9606;
 RN [1] -!
 DR SEQUENCE FROM N.A.
 RR Reed W., Moats-Staats B.M., Carson J.L., Leigh M.W., Collier A.M.;
 RR "A ciliary dynein heavy chain whose expression is upregulated in differentiating airway epithelium";
 RR Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 DR SEQUENCE FROM N.A.
 RR TISSUE=Nasal epithelium;
 RR Carrolloni L., Blouin J.L., Maiti A., Sainsbury A., Rossier C., Gehrig C., She J.X., Marron M.P., Lander E., Meeks M., Chung E., Jorissen M., Scott H.S., Delozier Blanchet C.D., Gardiner M., Antonarakis S.E.;
 RR "Axonemal beta heavy chain dynein DNA19: cDNA sequence, genomic structure and investigation of its role in primary ciliary dyskinesia";
 RR Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 DR SEQUENCE OF 1874-1974 FROM N.A.
 RR Tissue=Nasal polyps;
 RR Maiti A.K., Mattel M.G., Jorissen M., Volz A., Ziegler A., Bouvagnet P.;
 RR "Chromosomal localization of human dynein heavy chain genes.";
 RR Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 DR CHARACTERIZATION,
 RR MEDLINE=2058134; PubMed=11104725;
 RR Reed W., Carson J.L., Moats-Staats B.M., Lucier T., Hu P.C., Brighton L., Gambling T.M., Huang C.H., Leigh M.W., Collier A.M.;
 RR "Characterization of an axonemal dynein heavy chain expressed early in airway epithelial ciliogenesis";
 RR Am. J. Respir. Cell Mol. Biol. 23:734-741(2000).
 DR -!- FUNCTION: FORCE GENERATING PROTEIN OF RESPIRATORY CILIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEN HAS ATPASE ACTIVITY.
 CC
 CC -!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.
 CC
 CC -!- SIMILARITY: BELONGS TO THE DYNEN HEAVY CHAIN FAMILY.
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 DR EMBL; AF257737; CAB94756.1; -
 DR EMBL; AJ132088; CA10561.1; -.

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